

24. An isolated PRO polypeptide lacking its associated signal peptide.
25. An isolated polypeptide having at least about 80% amino acid sequence identity to an extracellular domain of of PRO polypeptide.
- 5 26. An isolated polypeptide having at least about 80% amino acid sequence identity to a PRO polypeptide lacking its associated signal peptide.
27. An isolated nucleic acid encoding the polypeptide of any one of Claims 23 to 26.

FIGURE 1

CCAATCGCCCGGTGCGGTGGTGCAGGGTCTCGGGCTAGTCAATGGCGTCCCCGTCTCGGAGAC
TGCAGACTAAACCAGTCATTACTTGTTTCAAGAGCGTTCTGCTAATCTACACTTTTATTTTC
TGGATCACTGGCGTTATCCTTCTTGCAAGTTGGCATTGTTGGGGCAAGGTGAGCCTGGAGAATTA
CTTTTCTCTTTTAAATGAGAAGGCCACCAATGTCCCCTTCGTGCTCATTGCTACTGGTACCG
TCATTATTCTTTTGGGCACCTTTGGTTGTTTTGCTACCTGCCGAGCTTCTGCATGGATGCTA
AAACTGTATGCAATGTTTCTGACTCTCGTTTTTTTTGGTTCGAACTGGTCGCTGCCATCGTAGG
ATTTGTTTTTCAAGCATGAGATTAAGAAGAGCTTTAAGAATAATTATGAGAAGGCTTTGAAGC
AGTATAACTCTACAGGAGATTATAGAAGCCATGCAGTAGACAAGATCCAAAATACGTTGCAT
TGTTGTGGTGTACCGATTATAGAGATTGGACAGATACTAATTATTACTCAGAAAAAGGATT
TCCTAAGAGTTGCTGTAACTTGAAGATTGTACTCCACAGAGAGATGCAGACAAAGTAAACA
ATGAAGGTTGTTTTATAAAGGTGATGACCATTATAGAGTCAGAAATGGGAGTCGTTGCAGGA
ATTTCTTTGGAGTTGCTTGCTTCCAAGTATTGGAATCTTTCTCGCCTACTGCCWCTCTCG
TGCCATAACAAATAACCAGTATGAGATAGTGTAACCCAATGTATCTGTGGGCCTATTCCTCT
CTACCTTTAAGGACATTTAGGGTCCCCCTGTGAATTAGAAAGTTGCTTGGCTGGAGAACTG
ACAACACTACTTACTGATAGACCAAAAACTACACCAGTAGGTTGATTCAATCAAGATGTAT
GTAGACCTAAACTACACCAATAGGCTGATTCAATCAAGATCCGTGCTCGCAGTGGGCTGAT
TCAATCAAGATGTATGTTTGCTATGTTCTAAGTCCACCTTCTATCCCATTCAATGTTAGATCG
TTGAAACCCTGTATCCCTCTGAAACACTGGAAGAGCTAGTAAATTGTAAATGAAGT

FIGURE 2

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA19902

><subunit 1 of 1, 245 aa, 1 stop, 1 unknown

><MW: -1, pI: 8.36, NX(S/T): 1

MASPSRRLQTKPVITCFKSVLLIYTFIFWITGVILLAVGIWGKVSLENYFSLLNEKATNVPF
VLIATGTVIILLGTFGCFATCRASAWMLKLYAMFLTLVFLVELVAAIVGFVFRHEIKNSFKN
NYEKALKQYNSTGDYRSHAVDKIQNTLHCCGVTDYRDWTDNYYSEKGFPSCKLEDCTPQ
RDADKVNNEGCFIKVMTIIESEMGVVAGISFGVACFQLIGIFLAYCXSRITNNQYEIV

Important features of the protein:

Signal peptide:

amino acids 1-42

Transmembrane domains:

amino acids 19-42, 61-83, 92-114, 209-230,

N-glycosylation site.

amino acids 134-138

Tyrosine kinase phosphorylation site.

amino acids 160-168, 160-169

N-myristoylation site.

amino acids 75-81, 78-84, 210-216, 214-220, 226-232

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 69-80, 211-222

FIGURE 3

CCCACGCGTCCGGCGCCGTGGCCTCGCGTCCATCTTTGCCGTTCTCTCGGACCTGTCACAAA
GGAGTCGCGCCGCCGCCGCCGCCCTCCCTCCGGTGGGCCCCGGGAGGTAGAGAAAGTCAGT
GCCACAGCCCGACCGCGCTGCTCTGAGCCCTGGGCACGCGGAACGGGAGGGAGTCTGAGGGT
TGGGGACGTCTGTGAGGGAGGGGAACAGCCGCTCGAGCCTGGGGCGGGCGGACCGGACTGGG
GCCGGGGTAGGCTCTGGAAAGGGCCCCGGGAGAGAGGTGGCGTTGGTCAGAACCTGAGAAACA
GCCGAGAGGTTTTCCACCGAGGCCCGCGCTTGAGGGATCTGAAGAGGTTCTAGAGAGGGT
GTTCCCTCTTTCCGGGGTCTCACCAGAAGAGGTTCTTGGGGTCCGCCCTCTGAGGAGGCT
GCGGCTAACAGGGCCCAGAACTGCCATTGGATGTCCAGAATCCCCTGTAGTTGATAATGTTG
GGAATAAGCTCTGCAACTTTCTTTGGCATTGAGTTGTTAAAAACAAATAGGATGCAAAATCC
TCAACTCCAGGTTATGAAAACAGTACTTGAAAACTGAAAACTACCTAAATGATCGTCTTTG
GTTGGGCCGTGTTCTTAGCGAGCAGAAGCCTTGGCCAGGGTCTGTTGTTGACTCTCGAAGAG
CACATAGCCCACTTCCTAGGGACTGGAGGTGCCGCTACTACCATGGGTAATTCCTGTATCTG
CCGAGATGACAGTGGAACAGATGACAGTGTGACACCCAACAGCAACAGGCCGAGAACAGTG
CAGTACCCACTGCTGACACAAGGAGCCAACCACGGGACCCTGTTCCGCCACCAAGGAGGGGC
CGAGGACCTCATGAGCCAAGGAGAAAGAAACAAATGTGGATGGGCTAGTGTTGGACACACT
GGCAGTAATACGGA CTCTGTAGATAAGTAAGTATCTGACTCACGGTCACCTCCAGTGGAAT
GAAAAGTGTTCTGCCCCGAACCATGACTTTAGGACTCCTTCAGTTCCTTTAGGACATACTCG
CCAAGCCTTGCTGCTCACAGGGCAAAGGAGAATATTTTAATGCTCCGCTGATGGCAGAGTAAA
TGATAAGATTTGATGTTTTTGCTTGCTGTCATCTACTTTGTCTGGAAATGTCTAAATGTTTC
TGTAGCAGAAAACACGATAAAGCTATGATCTTTATTAGAG

FIGURE 4

MIVFGWAVFLASRLGQGLLLTLEEHIAHFLGTGGAATTMGNSCICRDDSGTDDSVDTQQQQ
AENSAVPTADTRSQPRDPVRPPRRGRGPHEPRRKKQNVDGLVLDLAVIRTLVDKO

Signal peptide:

amino acids 1-16

Casein kinase II phosphorylation site.

amino acids 22-26, 50-54, 113-117

N-myristoylation site.

amino acids 18-24, 32-38, 34-40, 35-41, 51-57

FIGURE 5

GGCACGAGGCGCTGTCCACCCGGGGGCGTGGGAGTGAGGTACCAGATTCAGCCCATTGCGC
CCGACGCCTCTGTTCTCGGAATCCGGGTGCTGCGGATTGAGGTCCCGGTTCTAACGGACTG
CAAGATGGAGGAAGGCGGGAACCTAGGAGGCCTGATTAAGATGGTCCATCTACTGGTCTTGT
CAGGTGCCTGGGGCATGCAAATGTGGGTGACCTTCGTCTCAGGCTTCCTGCTTTTCCGAAGC
CTTCCCCGACATACCTTCGGACTAGTGCAGAGCAAACCTTTCCCCTTCTACTTCCACATCTC
CATGGGCTGTGCCTTCATCAACCTCTGCATCTTGGCTTCACAGCATGCTTGGGCTCAGCTCA
CATTCTGGGAGGCCAGCCAGCTTTACCTGCTGTTCTTGAGCCTTACGCTGGCCACTGTCAAC
GCCCCGCTGGCTGGAACCCCGCACCACAGCTGCCATGTGGGCCCTGCAAACCGTGGAGAAGGA
GCGAGGCCTGGGTGGGGAGGTACCAGGCAGCCACCAGGGTCCCGATCCCTACCGCCAGCTGC
GAGAGAAGGACCCCAAGTACAGTGCTCTCCGCCAGAATTTCTTCCGCTACCATGSGCTGTCC
TCTCTTTGCAATCTGGGCTGCGTCCTGAGCAATGGGCTCTGTCTCGCTGGCCTTGCCCTGGA
AATAAGGAGCCTCTAGCATGGGCCCTGCATGCTAATAAATGCTTCTTCAGAAATGAAAAAA
AAAAAAAAAAAA

FIGURE 6

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56107

<subunit 1 of 1, 231 aa, 1 stop

<NX(S/T): 0

MEEGGNLGGLIKMVHLLVLSGAWGMQMWVTFVSGFLLFRSLPRHTFGLVQSKLFPFYFHISM
GCAFINLCILASQHAWAQLTFWEASQLYLLFSLTLATVNAWLEPRTTAAMWALQTVEKER
GLGGEVPGSHQGPDPYRQLREKDPKYSALRQNFFRYHGLSSLCNLGCVLSNGLCLAGLALEIRSL

Signal peptide:

amino acids 1-24

Transmembrane domain:

amino acids 86-103, 60-75

Casein kinase II phosphorylation site.

amino acids 82-86

Tyrosine kinase phosphorylation site.

amino acids 144-151

N-myristoylation site.

amino acids 4-10, 5-11, 47-53, 170-176, 176-182

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 54-65

G-protein coupled receptors proteins.

amino acids 44-85

FIGURE 7

AATTCAGATTTTAAGCCCATTCCTGCAGTGGAATTTTCATGAACTAGCAAGAGGACACCATCTT
CTTGTATTATACAAGAAAGGAGTGACCTATCACACACAGGGGGAAAAATGCTCTTTTGGGT
GCTAGGCCTCCTAATCCTCTGTGGTTTTCTGTGGACTCGTAAAGGAAACTAAAGATTGAAG
ACATCACTGATAAGTACATTTTTATCACTGGATGTGACTCGGGCTTTGGAACTTGGCAGCC
AGAACTTTTGATAAAAAGGGATTTTCATGTAATCGCTGCCTGTCTGACTGAATCAGGATCAAC
AGCTTTAAAGGCAGAAACCTCAGAGAGACTTCGTA CTGTGCTTCTGGATGTGACCGACCCAG
AGAATGTCAAGAGGACTGCCCAGTGGGTGAAGAACCAAGTTGGGGAGAAAGGTCTCTGGGGT
CTGATCAATAATGCTGGTGTTCCCGGCGTGCTGGCTCCCACTGACTGGCTGACACTAGAGGA
CTACAGAGAACCTATTGAAGTGAACCTGTTTGGACTCATCAGTGTGACACTAAATATGCTTC
CTTTGGTCAAGAAAGCTCAAGGGAGAGTTATTAATGTCTCCAGTGTTGGAGGTCCTCTTGCA
ATCGTTGGAGGGGGCTATACTCCATCCAAATATGCAGTGGAAGGTTTCAATGACAGCTTAAG
ACGGGACATGAAAGCTTTTGGTGTGCACGTCTCATGCATTGAACCAGGATTGTTCAAAACAA
ACTTGGCAGATCCAGTAAAGGTAATTGAAAAAACTCGCCATTTGGGAGCAGCTGTCTCCA
GACATCAACAACAATATGGAGAAGGTTACATTGAAAAAGTCTAGACAACTGAAAGGCAA
TAAATCCTATGTGAACATGGACCTCTCTCCGGTGGTAGAGTGCATGGACCACGCTCTAACAA
GTCTCTTCCCTAAGACTCATTATGCCGCTGGAAAAGATGCCAAAATTTTCTGGATACCTCTG
TCTCACATGCCAGCAGCTTTGCAAGACTTTTTATTGTTGAAACAGAAAGCAGAGCTGGCTAA
TCCCAAGGCAGTGTGACTCAGCTAACCACAAATGTCTCCTCCAGGCTATGAAATTGGCCGAT
TTCAAGAACACATCTCCTTTTCAACCCCATTCCTTATCTGCTCCAACCTGGACTCATTTAGA
TCGTGCTTATTTGGATTGCAAAAGGGAGTCCCACCATCGCTGGTGGTATCCAGGGTCCCTG
CTCAAGTTTTCTTTGAAAAGGAGGGCTGGAATGGTACATCACATAGGCAAGTCTGCCCCTGT
ATTTAGGCTTTGCCTGCTTGGTGTGATGTAAGGGAAATTGAAAGACTTGCCCATTCAAAATG
ATCTTTACCGTGGCCTGCCCCATGCTTATGGTCCCCAGCATTTACAGTAACTTGTGAATGTT
AAGTATCATCTCTTATCTAAATATTAAGATAAGTCAACCCAAAAAAAAAAAAAAAAAAAAA
AAAAAAAAAAAAAAAAAAAAA

FIGURE 8

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56406

><subunit 1 of 1, 319 aa, 1 stop

><MW: 35227, pI: 8.97, NX(S/T): 3

MLFWVLGLLLILCGFLWTRKGKLIKIEDITDKYIFITGCDSGFGNLAARTFDKKGFHVIAACLT
ESGSTALKAETSERLRTVLLDVTDPENVKRTAQWVKNQVGEKGLWGLINNAGVPGVLAPTDW
LTLEDYREPIEVNLFGLISVTLNMLPLVKKAQGRVINVSSVGGRLAIVGGGYTPSKYAVEGF
NDSLRRDMKAFGVHVSCEPGLFKTNLADPVKVIEWKKLAIWEQLSPDIKQQYGEGYIEKSLD
KLKGNKSYVNMDLSPVVECMDHALTSLFPKTHYAAGKDAKIFWIPLSHMPAALQDFLLKQK
AELANPKAV

Important features of the protein:

Signal peptide:

amino acids 1-17

Transmembrane domain:

amino acids 136-152

N-glycosylation sites.

amino acids 161-163, 187-190 and 253-256

Glycosaminoglycan attachment site.

amino acids 39-42

N-myristoylation sites.

amino acids 36-41, 42-47, 108-113, 166-171, 198-203 and 207-212

FIGURE 9

GCGGGCTGTTGACGGCGCTGCGATGGCTGCCTGCGAGGGCAGGAGAAGCGGAGCTCTCGGTT
CCTCTCAGTCGGACTTCCTGACGCCGCCAGTGCGCGGGGCCCTTGGGCCGTGCCACCACT
GTAGTCATGTACCCACCGCCGCCGCCGCCCTCATCGGGACTTCATCTCGGTGACGCTGAG
CTTTGGCGAGAGCTATGACAACAGCAAGAGTTGGCGGGCGGCTCGTGCTGGAGGAAATGGA
AGCAACTGTCGAGATTGCAGCGGAATATGATTCTCTTCTCCTTGCCTTTCTGCTTTTCTGT
GGACTCCTCTTCTACATCAACTTGGCTGACCATTGGAAAGCTCTGGCTTTTCAGGCTAGAGGA
AGAGCAGAAGATGAGGCCAGAAATTGCTGGGTAAAACAGCAAATCCACCCGTCTTACCAG
CTCCTCAGAAGGCGGACACCGACCCTGAGAACTTACCTGAGATTTCTGTACAGAAGACACAA
AGACACATCCAGCGGGGACCACCTCACCTGCAGATTAGACCCCAAGCCAAGACCTGAAGGA
TGGGACCCAGGAGGAGGCCACAAAAGGCAAGAAGCCCTGTGGATCCCCGCCCGGAAGGAG
ATCCGCAGAGGACAGTCATCAGCTGGAGGGGAGCGGTGATCGAGCCTGAGCAGGGCACCGAG
CTCCCTTCAAGAAGAGCAGAAGTGCCACCAAGCCTCCCCTGCCACCGGCCAGGACACAGGG
CACACCAGTGCATCTGAACTATCGCCAGAAGGGCGTGATTGACGTCTTCTGTCATGCATGGA
AAGGATACCGCAAGTTTGCATGGGGCCATGACGAGCTGAAGCCTGTGTCCAGGTCTTTCAGT
GAGTGGTTTGGCCTCGGTCTCACACTGATCGACGCGCTGGACACCATGTGGATCTTGGGTCT
GAGGAAAGAATTTGAGGAAGCCAGGAAGTGGGTGTGGAAGAAGTTACACTTTGAAAAGGACG
TGGACGTCAACCTGTTTGAAGAGCACGATCCGCATCCTGGGGGGGCTCCTGAGTGCCTACCAC
CTGTCTGGGGACAGCCTCTTCTGAGGAAAGCTGAGGATTTTGGAAATCGGCTAATGCCTGC
CTTCAGAACACCATCCAAGATTCCTTACTCGGATGTGAACATCGGTACTGGAGTTGCCACCC
CGCCACGGTGGACCTCCGACAGCACTGTGGCCGAGGTGACCAGCATTCAGCTGGAGTTCCGG
GAGCTCTCCCGTCTCACAGGGGATAAGAAGTTTCAGGAGGCAGTGGAGAAGGTGACACAGCA
CATCCACGGCCTGTCTGGGAAGAAGGATGGGCTGGTGCCCATGTTTCATCAATACCCACAGTG
GCCTCTTACCCACCTGGGCGTATTCACGCTGGGCGCCAGGGCCGACAGCTACTATGAGTAC
CTGCTGAAGCAGTGGATCCAGGGCGGGAAGCAGGAGACACAGCTGCTGGAAGACTACGTGGA
AGCCATCGAGGGTGTGAGAACGCACCTGCTGCGGCACTCCGAGCCCAGTAAGCTCACCTTTG
TGGGGGAGCTTGCCACGGCCGCTTTCAGTGCCAAGATGGACCACCTGGTGTGCTTCTGCCA
GGGACGCTGGCTCTGGGCGTCTACCACGGCCTGCCCGCCAGCCACATGGAGCTGGCCAGGA
GCTCATGGAGACTTGTTACCAGATGAACCGGCAGATGGAGACGGGGCTGAGTCCCGAGATCG
TGCACTTCAACCTTTACCCCCAGCCGGGCGTCCGGACGTGGAGGTCAAGCCAGCAGACAGG
CACAACTGCTGCGGCCAGAGACCGTGGAGAGCCTGTTCTACCTGTACCGCTCACAGGGGA
CCGCAAATACCAGGACTGGGGCTGGGAGATTCTGCAGAGCTTCAGCCGATTCACACGGGTCC
CCTCGGGTGGCTATTCTTCCATCAACAATGTCCAGGATCCTCAGAAGCCCAGCCTAGGGAC
AAGATGGAGAGCTTCTTCTGGGGGAGACGCTCAAGTATCTGTTCTTGCTCTTCTCCGATGA
CCCAAACCTGCTCAGCCTGGACGCCTACGTGTTCAACACCGAAGCCCACCTCTGCCTATCT
GGACCCCTGCCCTAGGGTGGATGGCTGCTGGTGTGGGGAATTCGGGTGGGCAGAGGCACCTTG
CTGGGTCTGTGGCATTTTCCAAGGGCCACGTAGCACCGGCAACCGCCAAGTGGCCAGGCT
CTGAACTGGCTCTGGGCTCCTCCTCGTCTCTGCTTTAATCAGGACACCGTGAGGACAAGTGA
GGCCGTGAGTCTTGGTGTGATGCGGGGTGGGCTGGGCCGCTGGAGCCTCCGCCTGCTTCTC
CAGAAGACACGAATCATGACTCACGATTGCTGAAGCCTGAGCAGGTCTCTGTGGGCCGACCA
GAGGGGGGCTTCGAGGTGGTCCCTGGTACTGGGGTGACCGAGTGGACAGCCCAGGGTGCAGC
TCTGCCCGGGCTCGTGAAGCCTCAGATGTCCCAATCCAAGGGTCTGGAGGGGCTGCCGTGA
CTCCAGAGGCCTGAGGCTCCAGGGCTGGCTCTGGTGTTTACAAGCTGGACTCAGGGATCCTC
CTGGCCGCCCGCAGGGGGGCTTGGAGGGCTGGACGGCAAGTCCGTCTAGCTCACGGGCCCT
CCAGTGGAATGGGTCTTTTCGGTGGAGATAAAAGTTGATTTGCTCTAACCGCAA

FIGURE 10

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56529

><subunit 1 of 1, 699 aa, 1 stop

><MW: 79553, pI: 7.83, NX(S/T): 0

MAACEGRRSGALGSSQSDFLTPPVGGAPWAVATTVMYPPPPPPPHRDFISVTLSFGESYDN
SKSWRRRSCWRKWKQLSRLQRNMILFLLAFLLFCGLLFYINLADHWKALAFRLEEEQKMRPE
IAGLKPANPPVLPAPQKADTDPENLPEISSQKTQRHIQRGPPHLQIRPPSQDLKDGTQEEAT
KRQEAPVDP RPPEGDPQRTVISWRGAVIEPEQGTELPSRRAEVPTKPPLPPARTQGTPVHLNY
RQKGVIDVFLHAWKGYRKFAWGHDELKPVSRSFSEWFGLGLTLIDALDTMWILGLRKEFEEA
RKWVSKKLHF EKDVDVNLFE STIRILGGLLSAYHLSGDSLFLRKAEDFGNRLMPAFRTPSKI
PYSDVNIGTGVAHPPRWTSDSTVAEVT SIQLEFRELSRLTGDKKFQEAVEKVTQMIHGLSGK
KDGLVPMFINTHSGLFTHLGVFTLGARADSYEYLLKQWIQGGKQETQLLEDYVEAIEGVRT
HLLRHSEPSKLT FVGELAHGRFSAKMDHLVCFLPGTLALGVYHGLPASHMELAQELMETCYQ
MNRQMETGLSPEIVHFNLYPQPGRRDVEVKPADRHNL RPETVESLFYLYRVTGDRKYQDWG
WEILQSFSRFRTRVPSGGYSSINNVQDPQKPEPRDKMESFFLGETLKYL FLLFSDDPNLLSLD
AYVFNTEAHPLPIWTPA

Important features of the protein:

Transmembrane domain:

amino acids 21-40 and 84-105 (type II)

FIGURE 11

GGCGCCGCGTAGGCCCGGGAGGCCGGGCCGGGCTGCGAGCGCCTGCCCCATGCGCCGC
CGCCTCTCCGCACGATGTTCCCCTCGCGGAGGAAAGCGGCGCAGCTGCCCTGGGAGGACGGC
AGGTCCGGGTTGCTCTCCGGCGGCCTCCCTCGGAAGTGTTCCGTCTTCCACCTGTTTCGTGGC
CTGCCTCTCGCTGGGCTTCTTCTCCCTACTCTGGCTGCAGCTCAGCTGCTCTGGGGACGTGG
CCCGGGCAGTCAGGGGACAAGGGCAGGAGACCTCGGGCCCTCCCGTGCCTGCCCCCAGAG
CCGCCCCCTGAGCACTGGGAAGAAGACGCATCCTGGGGCCCCACCGCCTGGCAGTGCTGGT
GCCCTTCCGCGAACGCTTCGAGGAGCTCCTGGTCTTCGTGCCCCACATGCGCCGCTTCCTGA
GCAGGAAGAAGATCCGGCACCATCTACGTGCTCAACCAGGTGGACCACTTCAGGTTCAAC
CGGGCAGCGCTCATCAACGTGGGCTTCCTGGAGAGCAGCAACAGCACGGACTACATTGCCAT
GCACGACGTTGACCTGCTCCCTCTCAACGAGGAGCTGGACTATGGCTTTCCTGAGGCTGGGC
CCTTCCACGTGGCCTCCCCGAGCTCCACCCTCTCTACCACTACAAGACCTATGTGCGCGGC
ATCCTGCTGCTCTCCAAGCAGCACTACCGGCTGTGCAATGGGATGTCCAACCGCTTCTGGGG
CTGGGGCCGCGAGGACGACGAGTTCTACCGGCGCATTAAGGGAGCTGGGCTCCAGCTTTTCC
GCCCCCTCGGGAATCACAACCTGGGTACAAGACATTTGCCACCTGCATGACCCAGCCTGGCGG
AAGAGGGACCAGAAGCGCATCGCAGCTCAAAAACAGGAGCAGTTCAAGGTGGACAGGGAGGG
AGGCCTGAACACTGTGAAGTACCATGTGGCTTCCCGCACTGCCCTGTCTGTGGGCGGGGCC
CCTGCACTGTCCTCAACATCATGTTGGACTGTGACAAGACCGCCACACCCTGGTGACATTTC
AGCTGAGCTGGATGGACAGTGAGGAAGCCTGTACCTACAGGCCATATTGCTCAGGCTCAGGA
CAAGGCCTCAGGTCGTGGGCCCAGCTCTGACAGGATGTGGAGTGGCCAGGACCAAGACAGCA
AGCTACGCAATTGCAGCCACCCGGCCGCAAGGCAGGCTTGGGCTGGGCCAGGACACGTGGG
GTGCCTGGGACGCTGCTTGCCATGCACAGTGATCAGAGAGAGGCTGGGGTGTGTCTGTCCG
GGACCCCCCTGCCTTCCTGCTCACCTACTCTGACCTCCTTCACGTGCCCAGGCCTGTGGG
TAGTGGGGAGGGCTGAACAGGACAACCTCTCATCACCTACTCTGACCTCCTTCACGTGCCC
AGGCCTGTGGGTAGTGGGGAGGGCTGAACAGGACAACCTCTCATCACCCCCAAAAAAAAAAAA
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FIGURE 12

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56531

><subunit 1 of 1, 327 aa, 1 stop

><MW: 37406, pI: 9.30, NX(S/T): 1

MFPSRRKAAQLPWEDGRSGLLSGGLPRKCSVFHLFVACLSLGFFSLLWLQLSCSGDVARAVR
GQGQETSGPPRACPPPEPPPEHWEEDASWGPHRLAVLVPFRERFEELLVFVPHMRRFLSRKKI
RHHIYVLNQVDHFRFNRAALINVGFLESSNSTDYIAMHDVDLLPLNEELDYGFPEAGPFHVA
SPELHPLYHYKTYVGGILLLSKQHYRLCNGMSNRFWGWGREDDFYRRIKGAGLQLFRPSGI
TTGYKTRHLDPAWRKRDQKRIAAQKQEQFKVDREGGLNTVKYHVASRTALSVGGAPCTVL
NIMLDCDKTATPWCTFS

Signal peptide:

amino acids 1-42

Transmembrane domain:

amino acids 29-49 (type II)

N-glycosylation site.

amino acids 154-158

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 27-31

Tyrosine kinase phosphorylation site.

amino acids 226-233

N-myristoylation site.

amino acids 19-25, 65-71, 247-253, 285-291, 303-309, 304-310

12/270

FIGURE 13

CAATGTTTGCCTATCCACCTCCCCCAAGCCCCTTTACCTATGCTGCTGCTAACGCTGCTGCT
GCTGCTGCTGCTGCTTAAAGGCTCATGCTTGGAGTGGGGACTGGTCGGTGCCCAGAAAGTCT
CTTCTGCCACTGACGCCCCCATCAGGGATTGGGCCTTCTTTCCCCCTTCCTTTCTGTGTCTC
CTGCCTCATCGGCCTGCCATGACCTGCAGCCAAGCCCAGCCCCGTGGGGAAGGGGAGAAAGT
GGGGGATGGCTAAGAAAGCTGGGAGATAGGGAACAGAAGAGGGTAGTGGGTGGGCTAGGGGG
GCTGCCTTATTTAAAGTGGTTGTTTATGATTCTTATACTAATTTATACAAAGATATTAAGGC
CCTGTTCAATTAAGAAATTGTTCCCTTCCCCTGTGTTCAATGTTTGTAAGATTGTTCTGTGT
AAATATGTCTTTATAATAAACAGTTAAAAGCTGAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 14

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56862

<subunit 1 of 1, 73 aa, 1 stop

<MW: 7879, pI: 7.21, NX(S/T): 0

MLLLTLLLLLLLLLKGSCLEWGLVGAQKVSSATDAPIRDWAFPPSFLCLLPAMTCSQAQ

PRGEGEKVGDG

Important features:

Signal peptide:

amino acids 1-15

Growth factor and cytokines receptors family:

amino acids 3-18

14/270

FIGURE 15

GGGACCCATGCGGCCGTGACCCCCGGCTCCCTAGAGGCCAGCGCAGCCGAGCGGACAAAG
GAGCATGTCCGCGCCGGGAAGGCCCGTCTCCGGCCGCCATAAGGCTCCGGTCGCCGCTGG
GCCCCGCGCCGCTCCTGCCCGCCCGGGCTCCGGGGCGGCCGCTAGGCCAGTGCGCCGCCG
CTCGCCCCGAGGCCCGGCCCGCAGCATGGAGCCACCCGGACGCCGGCGGGGGCCGCGCGCA
GCCGCCGCTGTTGCTGCCGCTCTCGCTGTTAGCGCTGCTCGCGCTGCTGGGAGGCGGCGGCG
GCGGCGGCGCCGCGGCGCTGCCCGCCGGCTGCAAGCACGATGGGCGGCCCGAGGGGCTGGC
AGGGCGGCGGGCGCCGCCGAGGGCAAGGTGGTGTGCAGCAGCCTGGAACCTCGCGCAGGTCCT
GCCCCAGATACTCTGCCCAACCGCACGGTCACCCTGATTCTGAGTAACAATAAGATATCCG
AGCTGAAGAATGGCTCATTTTCTGGGTAAAGTCTCCTTGAAAGATTGGACCTCCGAAACAAT
CTTATTAGTAGTATAGATCCAGGTGCCTTCTGGGGACTGTCATCTCTAAAAAGATTGGATCT
GACAAACAATCGAATAGGATGTCTGAATGCAGACATATTTGAGGACTCACCAATCTGGTTC
GGCTAAACCTTTTCGGGAATTTGTTTTCTTCATTATCTCAAGGAACCTTTTGATTATCTTGCG
TCATTACGGTCTTTGGAATTCAGACTGAGTATCTTTGTGTGACTGTAACTACTGTGGAT
GCATCGCTGGGTAAAGGAGAAGAACATCACGGTACGGGATACCAGGTGTGTTTATCCTAAGT
CACTGCAGGCCCAACCAGTCACAGGCGTGAAGCAGGAGCTGTTGACATGCGACCCCTCCGCTT
GAATTGCCGTCTTTCTACATGACTCCATCTCATCGCCAAGTTGTGTTTGAAGGAGACAGCCT
TCCTTTCCAGTGCATGGCTTCATATATTGATCAGGACATGCAAGTGTTGTGGTATCAGGATG
GGAGAATAGTTGAAACCGATGAATCGCAAGGTATTTTGTGTTGAAAAGAACATGATTCACAAC
TGCTCCTTGATTGCAAGTGCCCTAACCATTTCTAATATTCAGGCTGGATCTACTGGAAATTG
GGGCTGTCTATGTCCAGACCAAACGTGGGAATAATACGAGGACTGTGGATATTGTGGTATTAG
AGAGTTCTGCACAGTACTGTCTCCAGAGAGGGTGGTAAACAACAAGGTGACTTCAGATGG
CCCAGAACATTGGCAGGCATTACTGCATATCTGCAGTGTACGCGGAACACCCATGGCAGTGG
GATATATCCCGGAAACCCACAGGATGAGAGAAAAGCTTGGCGCAGATGTGATAGAGGTGGCT
TTTGGGCAGATGATGATTATTCTCGCTGTCAGTATGCAAAATGATGTCCTAGAGTTCTTTAT
ATGTTTAATCAGATGCCCCCTCAATCTTACCAATGCCGTGGCAACAGCTCGACAGTTACTGGC
TTACACTGTGGAAGCAGCCAACCTTTTCTGACAAAATGGATGTTATATTGTGGCAGAAATGA
TTGAAAAATTTGGAAGATTTACCAAGGAGGAAAAATCAAAAGAGCTAGGTGACGTGATGGTT
GACATTGCAAGTAACATCATGTTGGCTGATGAACGTGTCTGTGGCTGGCGCAGAGGGAAGC
TAAAGCCTGCAGTAGGATTGTGCAGTGTCTTCAGCGCATTGCTACCTACCGGCTAGCCGGTG
GAGCTCACGTTTATTCAACATATTCACCCAATATTGCTCTGGAAGCTTATGTCATCAAGTCT
ACTGGCTTCACGGGGATGACCTGTACCGTGTTCCAGAAAGTGGCAGCCTCTGATCGTACAGG
ACTTTTCGATTATGGGAGGCGGGATCCAGAGGGAACCTGGATAAGCAGCTGAGCTTTAAGT
GCAATGTTTCAAATACATTTTCGAGTCTGGCACTAAAGGTATGTTACATTCTGCAATCATTT
AAGACTATTTACAGTTAAATTAGAATGCTCCAAATGTTCTGCTTCGCAAAATAACCTTATTA
AAAGATTTTTTTTGCAGGAAGATAGGTATTATTGCTTTTGCTACTGTTTTAAAGAAACTA
ACCAGGAAGAACTGCATTACGACTTTCAAGGGCCCTAGGCATTTTTGCCTTTGATTCCCTTT
CTTCACATAAAAAATATCAGAAATTACATTTTATAACTGCAGTGGTATAAATGCAATATACT
ATTGTTACATGTGAAAAATTTTATTTGACTTAAAAGTTTATTTATTTGTTTTTTTGCTCCT
GATTTTAAGACAATAAGATGTTTTCATGGGCCCTAAAAGTATCATGAGCCTTTGGCACTGC
GCCTGCCAAGCCTAGTGGAGAAGTCAACCCTGAGACCAGGTGTTTAATCAAGCAAGCTGTAT
ATCAAAATTTTTTGGCAGAAAACACAAATATGTCATATATCTTTTTTTTAAAAAAAGTATTTCA
TTGAAGCAAGCAAAATGAAAGCATTTTTACTGATTTTTAAATTTGGTGCTTTAGATATATTT
GACTACACTGTATTGAAGCAATAGAGGAGGCACAACTCCAGCACCTAATGGAACACATTT
TTTTTCACTTAGCTTTCTGTGGGCATGTGTAATTGTATTCTCTGCGTTTTTAATCTCACAG
TACTTTATTTCTGTCTTGTCCCTCAATAATATCAAAACAATATTCCAGTCATTTTAATGGC
TGCATAATAACTGATCCAACAGGTGTTAGGTGTTCTGGTTTAGTGTGAGCACTCAATAAATA
TTGAATGAATGAACGAAAAAAAAAAAAAAAAA

FIGURE 16

MEPPGRRRRGRAQPPLLLPLSLLALLALLGGGGGGGAAALPAGCKHDGRPRGAGRAAGAAEGK
VVCSSLELAQVLPPDTLPNRTVTLILSNNKISELKNGSFSGLSLLERLDLRNNLISSIDPGA
FWGLSSLKRLDLTNNRIGCLNADIFRGLTNLVRLNLSGNLFSSLSQGTFDYLA SLRSLEFQT
EYLLCDCNILWMHRWVKEKNITVRDTRCVYPKSLQAQPVTVGVKQELLTCDPPELPSFYMTF
SHRQVVFEGDSLPPFQCMASYIDQDMQVLWYQDGRIVETDESQGIFVEKNMIHNCSLIASALT
ISNIQAGSTGNWVGCHVQTKRGNNTRTVDIVVLESSAQYCPPERVVNNKGD FRWPRTLAGITA
YLQCTRNTHGSGIYPGNPQDERKAWRRCDRGGFWADDDYSRCQYANDVTRVLYMFNQ MPLNL
TNAVATARQLLAYTVEAANFSDKMDVIFVAEMIEKFGRFTKEEKS KELGDMVDIASNIMLA
DERVLWLAQREAKACSRIVQCLQRIATYRLAGGAHVYSTYSPNIALEAYVIKSTGFTGMTCT
VFQKVAASDRTGLSDYGRRDPEGNLDKQLSFKCNVSNTFSSSLALKVCYILQSFKTIYS

Signal peptide:

amino acids 1-33

Transmembrane domain:

amino acids 13-40 (type II)

N-glycosylation site.amino acids 81-85, 98-102, 159-163, 206-210, 301-305, 332-336,
433-437, 453-457, 592-596**N-myristoylation site.**amino acids 29-35, 30-36, 31-37, 32-38, 33-39, 34-40, 51-57,
57-63, 99-105, 123-129, 142-148, 162-168, 317-323, 320-326,
384-390, 403-409, 554-560

FIGURE 17

CGGTGGGGATGTCTAGGAGCTCGAAGGTGGTGCTGGGCCTCTCGGTGCTGCTGACGGCGGCC
ACAGTGGCCGGCGTACATGTGAAGCAGCAGTGGGACCAGCAGAGGCTTCGTGACGGAGTTAT
CAGAGACATTGAGAGGCAAATTCGGAAAAAAGAAAACATTCGTCTTTTGGGAGAACAGATTA
TTTTGACTGAGCAACTTGAAGCAGAAAGAGAGAAGATGTTATTGGCAAAGGATCTCAAAAA
TCATGACTTGAATGTGAAATATCTGTTGGACAGACAACACGAGTTTGTGTGTGTGTGTTGAT
GGAGAGTAGCTTAGTAGTATCTTCATCTTTTTTTTTTGGTCACTGTCCTTTTAAACTTGATCA
AATAAAGGACAGTGGGTCATATAAGTTACTGCTTTCAGGGTCCCTTATATCTGAATAAAGGA
GTGTGGGCAGACACTTTTTGGAAGAGTCTGTCTGGGTGATCCTGGTAGAAGCCCCATTAGGG
TCACTGTCCAGTGCTTAGGGTTGTTACTGAGAAGCACTGCCGAGCTTGTGAGAAGGAAGGGA
TGGATAGTAGCATCCACCTGAGTAGTCTGATCAGTCGGCATGATGACGAAGCCACGAGAACA
TCGACCTCAGAAGGACTGGAGGAAGGTGAAGTGGAGGGAGAGACGCTCCTGATCGTCGAATCC

FIGURE 18

MSRSSKVVLGLSVLLTAATVAGVHVKKQWDQQLRDGVIRDIERQIRKKENIRLLGEQIILT
EQLEAEREKMLLAKGSQKS

Signal peptide:
amino acids 1-21

FIGURE 19

CTGTCGTCTTTGCTTCAGCCGCAGTCGCCACTGGCTGCCTGAGGTGCTCTTACAGCCTGTTC
CAAGTGTGGCTTAATCCGTCTCCACCACCAGATCTTTCTCCGTGGATTCCCTCTGCTAAGACC
GCTGCCATGCCAGTGACGGTAACCCGCACCACCATCACAACCACCACGACGTCATCTTCGGG
CCTGGGGTCCCCCATGATCGTGGGGTCCCCTCGGGCCCTGACACAGCCCCTGGGTCTCCTTCGC
CTGCTGCAGCTGGTGTCTACCTGCGTGGCCTTCTCGCTGGTGGCTAGCGTGGGCGCCTGGAC
GGGGTCCATGGGCAACTGGTCCATGTTACCTGGTGTCTTGCTTCTCCGTGACCCTGATCA
TCCTCATCGTGGAGCTGTGCGGGCTCCAGGCCCGCTTCCCCCTGTCTTGCGCAACTTCCCC
ATCACCTTCGCCTGCTATGCGGCCCTCTTCTGCCTCTCGGCCCTCCATCATCTACCCACCAC
CTATGTCCAGTTCCTGTCCACGGCCGTTTCGCGGGACCACGCCATCGCCGCCACCTTCTTCT
CCTGCATCGCGTGTGTGGCTTACGCCACCGAAGTGGCCTGGACCCGGGCCCCGGCCCGGCGAG
ATCACTGGCTATATGGCCACCGTACCCGGGCTGCTGAAGGTGCTGGAGACCTTCGTTGCCTG
CATCATCTTCGCGTTCATCAGCGACCCCAACCTGTACCAGCACCAGCCGGCCCTGGAGTGGT
GCGTGGCGGTGTACGCCATCTGCTTCATCCTAGCGGCCATCGCCATCCTGCTGAACCTGGGG
GAGTGCACCAACGTGCTACCCATCCCCTTCCCCAGCTTCCTGTGCGGGCTGGCCTTGCTGTC
TGTCCTCCTCTATGCCACCGCCCTTGTTCTCTGGCCCCCTTACCAGTTCGATGAGAAGTATG
GCGGCCAGCCTCGGCGCTCGAGAGATGTAAGCTGCAGCCGCAGCCATGCCTACTACGTGTGT
GCCTGGGACCGCCGACTGGCTGTGGCCATCCTGACGGCCATCAACCTACTGGCGTATGTGGC
TGACCTGGTGCACCTCTGCCCACCTGGTTTTTGTCAAGGTCTTAAGACTCTCCCAAGAGGCTCC
CGTTCCTCTCCAACCTCTTTGTTCTTCTTGCCCGAGTTTTCTTTATGGAGTACTTCTTTCC
TCCGCCTTTCTCTGTTTTCTCTTCTGTCTCCCCTCCCTCCACCTTTTTCTTTCTTTCC
CAATTCCTTGCACTCTAACCAGTTCCTTGGATGCATCTTCTTCCCTTCCCTTCTCTTGCTGT
TTCTTCTCTGTGTTGTTTTGTTGCCACATCCTGTTTTTACCCTGAGCTGTTTCTTTTTT
CTTTTCTTTCTTTTTTTTTTTTTTTTTTAAAGACGGATTCTCACTCTGTGGCCCAGGCTGGAG
TGCAGTGGTGCATCTCAGCTCACTGCAACCCCCGCCTCCTGGGTTCAAGCGATTCTCCTCC
CCCAGCCTCCCAAGTAGCTGGGAGGACAGGTGTGAGCTGCCGCACCCAGCCTGTTTCTCTTT
TTCCACTCTTCTTTTTTCTCATCTCTTTTCTGGGTGTCCTGTGCGCTTCTTATCTGCCTGT
TTTGCAAGCACCTTCTCCTGTGTCTTGGGAGCCCTGAGACTTCTTCTCTCCTTGCTCCA
CCCACCTCCAAAGGTGCTGAGCTCACATCCACACCCCTTGACCCGTCCATGCCACAGCCCC
CCAAGGGGCCCCATTGCCAAAGCATGCCTGCCCACCCTCGCTGTGCCTTAGTCAGTGTGTAC
GTGTGTGTGTGTGTGTGTTGGGGGGTGGGGGGTGGGTAGCTGGGGATTGGGCCCTCTTTCT
CCCAGTGGAGGAAGGTGTGAGTGTACTTCCCCTTTAAATTAAAAACATATATATATATAT
ATTTGGAGGTGAGTAATTTCCAATGGGCGGGAGGCATTAAGCACCGACCCTGGGTCCCTAGG
CCCCGCCTGGCACTCAGCCTTGCCAGAGATTGGCTCCAGAATTTTGCCAGGCTTACAGAACAC
CCACTGCCTAGAGGCCATCTTAAAGGAAGCAGGGGCTGGATGCCTTTCATCCCACTATTCT
CTGTGGTATGAAAAAG

FIGURE 20

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA58727

<subunit 1 of 1, 322 aa, 1 stop

<MW: 35274, pI: 8.57, NX(S/T): 1

MPVTVTRTTTITTTTSSSGLGSPMIVGSPRALTQPLGLLRLLQLVSTCVAFSLVASVGAWTG
SMGNWSMFTWCFCFSVTLIILIVELCGLQARFPLSWRNFPITFACYAALFCLSASIIYPTTY
VQFLSHGRSRDHAIATFFSCIACVAYATEVAWTRARPGEITGYMATVPGLLKVLETFVACI
IFAFISDPNLYQHQPALWCVAVYAICFILAAIAILLNLGECTNVLPPIPFPSFLSGLALLSV
LLYATALVLWPLYQFDEKYGGQPRRSRDVSCSRSHAYYVCAWDRRLAVAILTAINLLAYVAD
LVHSAHLVFVKV

Important features:

Transmembrane domains:

amino acids 41-60 (type II), 66-85, 101-120, 137-153, 171-192,
205-226, 235-255 and 294-312

N-glycosylation site.

amino acids 66-69

Glycosaminoglycan attachment site.

amino acids 18-21

20/270

[illegible]

FIGURE 22

MFLATLSFLLPFAHPFGTVSCEYMLGSPLSSLAQVNLSPFSPKVMHMDPNYCHPSTSLHLCS
LAWSFTRLLHPPLSPGISQVVKDHVTKPTAMAQGRVAHLIEWKGWSKPSDSPAALSAFSSY
SDLSEGEQEARFAAGVAEQFAIAEAKLRAWSSVDGEDSTDDSYDEDFAGGMDTDMAGQLPLG
PHLQDLFTGHRFSRPVRQGSVEPESDCSQTVSPDTLCSSLCSLEDGLLGSPARLASQLLGDE
LLLAKLPPSRESAFRSLGPLEAQDSLNSPLTESCLSPAEEEEPAPCKDCQPLCPPLTGSWER
QRQASDLASSGVVSLDEDEAEPEEQ

Signal peptide:

amino acids 1-15

Casein kinase II phosphorylation site.amino acids 123-127, 128-132, 155-159, 162-166, 166-170, 228-232,
285-289, 324-328**Tyrosine kinase phosphorylation site.**

amino acids 44-52

N-myristoylation site.

amino acids 17-23, 26-32, 173-179

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 11-22

FIGURE 23

GGTTCCTGGGCGCTCTGTTACACAAGCAAGATACAGCCAGCCCCACCTAATTTTGTTCCTT
GGCACCCCTCCTGCTCAGTGCGACATTGTCACTTAACCCATCTGTTTTCTCTAATGCACGA
CAGATTCCCTTCAGACAGGACAACCTGTGATATTTAGTTCTTGATTGTAAATACCTCCTAAG
CCTGAAGCTTCTGTTACTAGCCATTGTGAGCTTCAGTTTCTTCATCTGCAAAATGGGCATAA
TACAATCTATTCTTGCCACATCAAGGGATTGTTATTCTTTAAAAAAAACCAATACCAAAG
AAGCCTACAATGTTGGCCTTAGCCAAAATTCTGTTGATTTCAACGTTGTTTTATTCACTTCT
ATCGGGGAGCCATGGAAAAGAAAATCAAGACATAAACACACAGAACATTGCAGAAGTTT
TTAAAACAATGGAAAATAAACCTATTTCTTTGGAAAGTGAAGCAAACCTTAACTCAGATAAA
GAAAATATAACCACCTCAAATCTCAAGGCGAGTCATTCCCCTCCTTTGAATCTACCCAACAA
CAGCCACGGAATAACAGATTTCTCCAGTAACTCATCAGCAGAGCATTCTTTGGGCAGTCTAA
AACCCACATCTACCATTTCCACAAGCCCTCCCTTGATCCATAGCTTTGTTTCTAAAGTGCCT
TGGAATGCACCTATAGCAGATGAAGATCTTTTGCCCATCTCAGCACATCCCAATGCTACACC
TGCTCTGTCTTCAGAAAACTTCACTGGTCTTTGGTCAATGACACCGTGAAAACCTCTGATA
ACAGTTCCATTACAGTTAGCATCCTCTCTTCAGAACCAACTTCTCCATCTGTGACCCCTTG
ATAGTGGAACCAAGTGGATGGCTTACCACAAACAGTGATAGCTTCACTGGGTTTACCCCTTA
TCAAGAAAAACAACCTCTACAGCCTACCTTAAAATTACCAATAATTCAAACTCTTTCCAA
ATACGTCAGATCCCCAAAAGAAAATAGAAATACAGGAATAGTATTCGGGGCCATTTTAGGT
GCTATTCTGGGTGTCTCATTGCTTACTCTTGTGGGCTACTTGTTGTGTGGAAAAGGAAAAC
GGATTCATTTTCCCATCGGCGACTTTATGACGACAGAAATGAACCAGTTCTGCGATTAGACA
ATGCACCGGAACCTTATGATGTGAGTTTTGGGAATTCTAGCTACTACAATCCAACCTTTGAAT
GATTCAGCCATGCCAGAAAGTGAAGAAAATGCACGTGATGGCATTCTATGGATGACATACC
TCCACTTCGTA CTCTGTATAGAACTAACAGCAAAAAGGCGTTAAACAGCAAGTGTCTCTA
CATCCTAGCCTTTTGACAAATTCTCTTTCAAAGGTTACACAAAATTACTGTCACGTGGAT
TTTGTCAAGGAGAATCATAAAAGCAGGAGACCAGTAGCAGAAATGTAGACAGGATGTATCAT
CCAAAGGTTTTCTTTCTTACAATTTTTGGCCATCCTGAGGCATTTACTAAGTAGCCTTAATT
TGTAATTTTAGTAGTATTTTCTTAGTAGAAAATATTTGTGGAATCAGATAAACTAAAAGATT
TCACCATTACAGCCCTGCCTCATAACTAAATAATAAAAATTATTCCACCAAAAAATTCTAAA
ACAATGAAGATGACTCTTTACTGCTCTGCCTGAAGCCCTAGTACCATAATTCAAGATTGCAT
TTTCTTAAATGAAAATTGAAAGGGTGCTTTTTTAAAGAAAATTTGACTTAAAGCTAAAAGAG
GACATAGCCCAGAGTTTCTGTTATTGGGAAATTGAGGCAATAGAAATGACAGACCTGTATTC
TAGTACGTTATAATTTCTAGATCAGCACACACATGATCAGCCCACTGAGTTATGAAGCTGA
CAATGACTGCATTCAACGGGGCCATGGCAGGAAAGCTGACCCTACCCAGGAAAGTAATAGCT
TCTTTAAAAGTCTTCAAAGGTTTTGGGAATTTTAACTTGTCTTAATATATCTTAGGCTTCAA
TTATTTGGGTGCCTTAAAACTCAATGAGAATCATGGT

FIGURE 24

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA58732

><subunit 1 of 1, 334 aa, 1 stop

><MW: 36294, pI: 4.98, NX(S/T): 13

MLALAKILLISTLFYSLLSGSHGKENQDINTTQNI AEVFKTMENKPISLESEANLNSDKENI
TTSNLKASHSPPLNLPNNSHGITDFSSNSSAEHSLGSLKPTSTISTSPPLIHSFVSKVPWNA
PIADEDLLPISAHPNATPALSSSENFTWLSLVNDTVKTPDNSSITVSILSSEPTSPSVTPLIVE
PSGWLTTNSDSFTGFTPYQEKTTLQPTLKFTNNSKLPNTSDPQKENRNTGIVFGAILGAIL
GVSLTLVGYLLCGKRKTD SFSHRRLYDDRNEPVLRLDNAPEPYDV SFGNSSYYNPTLNDSA
MPSEENARDGIPMDDIPPLRTSV

Signal peptide:

amino acids 1-23

Transmembrane domain:

amino acids 235-262

N-glycosylation site.

amino acids 30-34, 61-65, 79-83, 90-94, 148-152, 155-159,
163-167, 218-222, 225-229, 298-302, 307-311

FIGURE 25

AACAGGATCTCCTCTTGCACTCTGCAGCCCAGGACGCTGATTCCAGCAGCGCCTTACCGCGC
AGCCCGAAGATTCACTATGGTGAAAATCGCCTTCAATACCCCTACCGCCGTGCAAAAGGAGG
AGGCGCGGCAAGACGTGGAGGCCCTCCTGAGCCGCACGGTCAGAACTCAGATACTGACCGGC
AAGGAGCTCCGAGTTGCCACCCAGGAAAAAGAGGGCTCCTCTGGGAGATGTATGCTTACTCT
CTTAGGCCTTTTCATTCATCTTGGCAGGACTTATTGTTGGTGGAGCCTGCATTTACAAGTACT
TCATGCCCAAGAGCACCATTTACCGTGGAGAGATGTGCTTTTTTGATTCTGAGGATCCTGCA
AATTCCCTTCGTGGAGGAGAGCCTAACTTCCTGCCTGTGACTGAGGAGGCTGACATTCGTGA
GGATGACAACATTGCAATCATTGATGTGCCTGTCCCCAGTTTCTCTGATAGTGACCCTGCAG
CAATTATTGATGACTTTGAAAAGGGAATGACTGCTTACCTGGACTTGTTGCTGGGGAAGTGC
TATCTGATGCCCCCTCAATACTTCTATTGTTATGCCTCCAAAAAATCTGGTAGAGCTCTTTGG
CAAACTGGCGAGTGGCAGATATCTGCCTCAAACCTTATGTGGTTCGAGAAGACCTAGTTGCTG
TGGAGGAAATTCGTGATGTTAGTAACCTTGGCATCTTTATTTACCAACTTTGCAATAACAGA
AAGTCCTTCCGCCTTCGTGCGAGAGACCTCTTGCTGGGTTTCAACAAACGTGCCATTGATAA
ATGCTGGAAGATTAGACACTTCCCCAACGAATTTATTGTTGAGACCAAGATCTGTCAAGAGT
AAGAGGCAACAGATAGAGTGTCTTGGTAATAAGAAGTCAGAGATTTACAATATGACTTTAA
CATTAAGGTTTATGGGATACTCAAGATATTTACTCATGCATTTACTCTATTGCTTATGCTTT
AAAAAAGGAAAAAAAAAAAAAACTACTAACCCTGCAAGCTCTTGTCAAATTTTAGTTTAAT
TGGCATTGCTTGTTTTTTGAACTGAAATTACATGAGTTTCATTTTTTCTTGCATTTATAG
GGTTTAGATTTCTGAAAGCAGCATGAATATATCACCTAACATCCTGACAATAAATCCATCC
GTTGTTTTTTTTGTTGTTTGTCTTTTCTTTTCTTTTAAAGTAAGCTCTTATTCATCTTATG
GTGGAGCAATTTTAAAATTTGAAATATTTTAAATTGTTTTTGAACTTTTTGTGTAAAATATA
TCAGATCTCAACATTGTTGGTTTCTTTTGTCTTTTCAATTTGTACAACCTTTCTTGAATTTAGA
AATTACATCTTTGCAGTTCTGTTAGGTGCTCTGTAATTAACCTGACTTATATGTGAACAATT
TTCATGAGACAGTCATTTTTAACTAATGCAGTGATTCTTTCTCACTACTATCTGTATTGTGG
AATGCACAAAATTGTGTAGGTGCTGAATGCTGTAAGGAGTTTAGGTTGTATGAATTCTACAA
CCCTATAATAAATTTTACTCTATACAAAAAAAAAAAAAAAAAAAAA

FIGURE 26

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA58828

<subunit 1 of 1, 263 aa, 1 stop

<MW: 29741, pI: 5.74, NX(S/T): 1

MVKIAFNTPTAVQKEEARQDVEALLSRTVRTQILTGKELRVATQEKEGSSGRCMLTLLGLSF
ILAGLIVGGACIYKYFMPKSTIYRGEMCFDSEDPANSLRGGEPNFLPVTEADIREDDNIA
IIDVPVPSFSDSDPAAIHDFEKGMTAYLDLLLGNCYLMPLNTSIVMPPKNLVELFGKLASG
RYLPQTYVVREDLVAVEEIRDVSNLGIFYQLCNRKSFRLRRRDLLLGFNKRAIDKCWKIR
HFPNEFIVETKICQE

Type II transmembrane domain:

amino acids 53-75

N-glycosylation site.

amino acids 166-170

Casein kinase II phosphorylation site.

amino acids 35-39, 132-136, 134-138

N-myristoylation site.

amino acids 66-72, 103-109

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 63-74

FIGURE 27

GGAGGAGGGAGGGCGGGCAGGCGCCAGCCCAGAGCAGCCCCGGGCACCAGCACGGACTCTCT
CTTCCAGCCCAGGTGCCCCCACTCTCGCTCCATTCTGGCGGGAGCACCCAGTCCTGTACGCC
AAGGAACTGGTCCTGGGGGCACCAATGGTTTCGGCGGCAGCCCCCAGCCTCCTCATCCTTCTG
TTGCTGCTGCTGGGGTCTGTGCCTGCTACCGACGCCCCTCTGTGCCCCCTGAAGGCCACGTT
CCTGGAGGATGTGGCGGGTAGTGGGGAGGCCGAGGGCTCGTCGGCCTCCTCCCCGAGCCTCC
CGCCACCCTGGACCCCGGCCCTCAGCCCCACATCGATGGGGCCCCAGCCACAACCCTGGGG
GGCCCATCACCCCCACCAACTTCCTGGATGGGATAGTGGACTTCTTCCGCCAGTACGTGAT
GCTGATTGCTGTGGTGGGCTCCCTGGCCTTTCTGCTGATGTTTCATCGTCTGTGCCGCGGTCA
TCACCCGGCAGAAGCAGAAGGCCTCGGCCTATTACCCATCGTCCTTCCCCAAGAAGAAGTAC
GTGGACCAGAGTGACCGGGCCGGGGGCCCCGGGCCTTCAGTGAGGTCCCCGACAGAGCCCC
CGACAGCAGGCCCGAGGAAGCCCTGGATTCTCCCGGCAGCTCCAGGCCGACATCTTGGCCG
CCACCCAGAACCTCAAGTCCCCCACCAGGGCTGCACTGGGCGGTGGGGACGGAGCCAGGATG
GTGGAGGGCAGGGGCGCAGAGGAAGAGGAGAAGGGCAGCCAGGAGGGGGACCAGGAAGTCCA
GGGACATGGGGTCCCAGTGGAGACACCAGAGGCGCAGGAGGAGCCGTGCTCAGGGGTCTTG
AGGGGGCTGTGGTGGCCGGTGAGGGCCAAGGGGAGCTGGAAGGGTCTCTCTTGTTAGCCCAG
GAAGCCCAGGGACCAGTGGGTCCCCCGAAAGCCCCTGTGCTTGACAGAGTGTCCACCCCAG
TGTCTAACAGTCCTCCCGGGCTGCCAGCCCTGACTGTGCGGGCCCCCAAGTGGTCACCTCCCC
GTGTATGAAAAGGCCTTCAGCCCTGACTGCTTCCTGACACTCCCTCCTTGGCCTCCCTGTGG
TGCCAATCCCAGCATGTGCTGATTCTACAGCAGGCAGAAATGCTGGTCCCCGGTGCCCCGGA
GGAATCTTACCAAGTGCCATCATCCTTCACCTCAGCAGCCCCAAAGGGCTACATCCTACAGC
ACAGCTCCCCTGACAAAAGTGAGGGAGGGCACGTGTCCCTGTGACAGCCAGGATAAAACATCC
CCCAAAGTGCTGGGATTACAGGCGTGAGCCACCGTGCCCGGCCCAACTACTTTTTTAAACA
GCTACAGGGTAAAATCCTGCAGCACCCACTCTGGAAAATACTGCTCTTAATTTTCTGAAGG
TGGCCCCCTGTTTCTAGTTGGTCCAGGATTAGGGATGTGGGGTATAGGGCATTTAAATCCTC
TCAAGCGCTCTCCAAGCACCCCCGGCCTGGGGGTGAGTTTCTCATCCCGCTACTGCTGCTGG
GATCAGGTTGAATGAATGGAACCTTTCCTGTCTGGCCTCCAAAGCAGCCTAGAAGCTGAGGG
GCTGTGTTTGAGGGGACCTCCACCCTGGGGAAGTCCGAGGGGCTGGGGAAGGGTTTCTGACG
CCCAGCCTGGAGCAGGGGGGCCCTGGCCACCCCCTGTTGCTCACACATTGTCTGGCAGCCTG
TGTCCACAATATTCGTCACTCCTCGACAGGGAGCCTGGGCTCCGTCTGCTTTAGGGAGGCT
CTGGCAGGAGGTCTCTCCCCCATCCCTCCATCTGGGGCTCCCCAACCTCTGCACAGCTCT
CCAGGTGCTGAGATATAATGCACCAGCACATAAACCTTTATTCCGGCCTGAAAAAAAAAAAA
AAGA

FIGURE 28

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA58852

><subunit 1 of 1, 283 aa, 1 stop

><MW: 29191, pI: 4.52, NX(S/T): 0

MVSAAAPSLILLLLLLLGSPATDARSVPLKATFLEDVAGSGEAEAGSSASSPSLPPPWTPAL
SPTSMGPQPTTLGGPSPTNFLDGIVDFFRQYVMLIAVVGSLAFLLMFIVCAAVITRQKQKA
SAYYPSSFPPKKKYVDQSDRAGGPRAFSEVPDRAPDSRPEEALDSSRQLQADILAATQNLKSP
TRALGGGDGARMVEGRGAEEEEKGSQEGDQEVQGHGVPVETPEAQEPCSGVLEGAVVAGE
GQGELEGSLLLAQEAQGPVGPPEPCACSSVHPSV

Signal peptide:

amino acids 1-25

Transmembrane domain:

amino acids 94-118

N-myristoylation site.

amino acids 18-24, 40-46, 46-52, 145-151, 192-198, 193-199,
211-217, 238-244, 242-248

FIGURE 29

GTGGACTCTGAGAAGCCCAGGCAGTTGAGGACAGGAGAGAGAAGGCTGCAGACCCAGAGGGA
GGGAGGACAGGGAGTTCGGAAGGAGGAGGACAGAGGAGGGCACAGAGACGCAGAGCAAGGGCG
GCAAGGAGGAGACCCTGGTGGGAGGAAGACACTCTGGAGAGAGAGGGGGCTGGGCAGAGATG
AAGTTCCAGGGGCCCCCTGGCCTGCCTCCTGCTGGCCCTCTGCCTGGGCAGTGGGGAGGCTGG
CCCCCTGCAGAGCGGAGAGGAAAGCACTGGGACAAATATTGGGGAGGCCCTTGGACATGGCC
TGGGAGACGCCCTGAGCGAAGGGGTGGGAAAGGCCATTGGCAAAGAGGCCGGAGGGGCAGCT
GGCTCTAAAGTCAGTGAGGCCCTTGGCCAAGGGACCAGAGAAGCAGTTGGCACTGGAGTCAG
GCAGGTTCCAGGCTTTGGCGCAGCAGATGCTTTGGGCAACAGGGTCGGGGAAGCAGCCCATG
CTCTGGGAAACACTGGGCACGAGATTGGCAGACAGGCAGAAGATGTCATTTCGACACGGAGCA
GATGCTGTCCGCGGCTCCTGGCAGGGGGTGCCTGGCCACAGTGGTGCTTGGGAAACTTCTGG
AGGCCATGGCATCTTTGGCTCTCAAGGTGGCCTTGGAGGCCAGGGCCAGGGCAATCCTGGAG
GTCTGGGGACTCCGTGGGTCCACGGATACCCCGGAAACTCAGCAGGCAGCTTTGGAATGAAT
CCTCAGGGAGCTCCCTGGGGTCAAGGAGGCAATGGAGGGCCACCAAACCTTTGGGACCAACAC
TCAGGGAGCTGTGGCCCAGCCTGGCTATGGTTCAGTGAGAGCCAGCAACCAGAATGAAGGGT
GCACGAATCCCCACCATCTGGCTCAGGTGGAGGCTCCAGCAACTCTGGGGGAGGCAGCGGC
TCACAGTCGGGCAGCAGTGGCAGTGGCAGCAATGGTGACAACAACAATGGCAGCAGCAGTGG
TGGCAGCAGCAGTGGCAGCAGCAGTGGCAGCAGCAGTGGCGGCAGCAGTGGCGGCAGCAGTG
GTGGCAGCAGTGGCAACAGTGGTGGCAGCAGAGGTGACAGCGGCAGTGAGTCCTCCTGGGGA
TCCAGCACCGGCTCCTCCTCCGGCAACCACGGTGGGAGCGGCGGAGGAAATGGACATAAACC
CGGGTGTGAAAAGCCAGGGAATGAAGCCCGCGGGAGCGGGGAATCTGGGATTCTAGGGCTTCA
GAGGACAGGGAGTTTCCAGCAACATGAGGGAAATAAGCAAAGAGGGCAATCGCCTCCTTGGG
GGCTCTGGAGACAATTATCGGGGGCAAGGGTCGAGCTGGGGCAGTGGAGGAGGTGACGCTGT
TGGTGGAGTCAATACTGTGAACTCTGAGACGTCTCCTGGGATGTTTAACTTTGACACTTTCT
GGAAGAATTTTAAATCCAAGCTGGGTTTTCATCAACTGGGATGCCATAAACAAGGACCAGAGA
AGCTCTCGCATCCCCTGACCTCCAGACAAGGAGCCACCAGATTGGATGGGAGCCCCCAGACT
CCCTCCTTAAACACCACCCTCTCATCTAATCTCAGCCCTTGCCCTTGAAATAAACCTTA
GCTGCCCCACAA
AAA

FIGURE 30

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA59212
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><subunit 1 of 1, 440 aa, 1 stop
```

><MW: 42208, pI: 6.36, NX(S/T): 1

MKFQGPLACLLLA LCLGSGEAGPLQSGEESTGTNIGEALGHGLGDALSEGVGKAIGKEAGGA
AGSKVSEALGQGTREAVGTGVRQVPFGAADALGNRVGEAAHALGNTGHEIGRQAEDVIRHG
ADAVRGSWQGVPGHSGAWETSGGHGIFGSQGGGGQQGNPGLGTPTWVHGYPGNSAGSFGM
NPQGAPWGQGGNGGPPNFGTNTQGAVAQPGYGSVRASNQNEGCTNPPPSGSSGGSSNSSGGGS
GSQSGSSGSGSNNDNNNGSSSSGSSSSGSSSSGSSSSGSSSSGSSSSGSSSGNSGGSRGDSGSESSW
GSSTGSSSGNHGGSGGGNGHKPGCEKPGNEARGSGESGIQGFRGQGVSSNMREISKEGNRL
GGSGDNRYRGQSSWSGSGGDAVGGVNTVNSETSPGMFNFDTFWKNFKSKLGFINWDAINKDQ
RSSRIP

Signal peptide:

amino acids 1-21

N-glycosylation site.

amino acids 265-269

Glycosaminoglycan attachment site.

amino acids 235-239, 237-241, 244-248, 255-259, 324-328, 388-392

Casein kinase II phosphorylation site.

amino acids 26-30, 109-113, 259-263, 300-304, 304-308

N-myristoylation site.

amino acids 17-23, 32-38, 42-48, 50-56, 60-66, 61-67, 64-70,
74-80, 90-96, 96-102, 130-136, 140-146, 149-155, 152-158,
155-161, 159-165, 163-169, 178-184, 190-196, 194-200, 199-205,
218-224, 236-242, 238-244, 239-245, 240-246, 245-251, 246-252,
249-252, 253-259, 256-262, 266-272, 270-276, 271-277, 275-281,
279-285, 283-289, 284-290, 287-293, 288-294, 291-297, 292-298,
295-301, 298-304, 305-311, 311-317, 315-321, 319-325, 322-328,
323-329, 325-331, 343-349, 354-360, 356-362, 374-380, 381-387,
383-389, 387-393, 389-395, 395-401

Cell attachment sequence.

amino acids 301-304

FIGURE 31

GACCGGTCCCTCCGGTCTGGATGTGCGGACTCTGCTGCAGCGAGGGCTGCAGGCCCGCCGGGCGGTGCTCACCG
TGCCCTGGCTGGTGGAGTTTCTCTCCTTTGCTGACCATGTTGTTCCCTTGCTGGAATATTACCGGGACATCTTCA
CTCTCCTGCTGCGCCTGCACCGAGCTTGGTGTGTGTCGAGGAGAGTGAGGGGAAGATGTGTTTCTGAAACAAGC
TGCTGCTACTTGCTGTCTGCGCTGGCTTTTCCAGATTCCACAGTCCCTGAGGACTTGTCTTTCTGGAAGAGG
GTCCCTCATATGCCTTTGAGGTGGACACAGTAGCCCCAGAGCATGGCTTGGACAATGCGCCTGTGGTGGACCAGC
AGCTGCTCTACACCTGCTGCCCTACATCGGAGAGCTCCGGAACCTGCTCGCTTCGTGGGTGTGAGGCAGTAGTG
GACGGAGTGGGGGCTTCATGAGGAAAATCACCCCCACCACTACCACCAGCCTGGGAGCCCAGCCTTCCCAGACCA
GCCAGGGGCTGCAGGCACAGCTCGCCCAGGCCCTTTTCCACAACAGCCGCCCTCCTTGCGCCGACCGTAGAGT
TCGTGGCAGAAAAGAAATTGGATCAAACCTGTGTCAAACATATCAAGGCTACACTGGTGGCAGATCTGGTGGCCAGG
CAGAGTCACTTCTCCAAGAGCAGCTGGTGACACAGGGAGAGGAAGGGGGAGACCCAGCCCAGCTGTTGGAGATCT
TGTGTTCCCAGCTGTGCCCTCACGGGGCCAGGCATTGGCCCTGGGGCGGGAGTTCTGTCAAAGGAAGAGCCCTG
GGGCTGTGCGGGCGCTGCTTCCAGAGGAGACCCCGCAGCCGTTCTGAGCAGTGCAGAGAACATTGCTGTGGGGC
TTGCAACAGAGAAAGCCTGTGCTTGGCTGTGAGCCAACATCACAGCACTGATCAGGAGGGAGGTGAAAGCAGCAG
TGAGTCGCACACTTCGAGCCCAGGGTCTGAACCTGTGCCCCGGGGGAGCGGAGGGGCTGCTCCCCGCCCTGAC
GTGCTCTCCTTGCCCGTGGGGCCACGGGACCCCTGACGAGGGAGTCTCCCCAGAGCATCTGGAACAGCTCCTAGGC
CAGCTGGGCCAGACGCTGCGGTGCCGCCAGTTCTGTGCCACCTGCTGAGCAGCATCTGGCAAAGTGCTCTGTG
GAGTTAGCTTCCCTCCTCGTTGCAGATCAAATTCCTATCCTAGGGCCCCCGGCACAGTACAGGCTGGAGAGAGGG
CAGGCTCGAAGGCTTCTGCACATGCTGCTTCCCTTGTTGAAGGAAGACTTTCAGGGGCCGGTTCGGCTGCAGCTG
CTGCTGAGCCCAAGAAATGTGGGGCTTCTGGCAGACACAAGGCCAAGGGAGTGGGACTTGCTGCTATTCTTGCTA
CGGGAGCTGGTGGAGAAGGGTCTGATGGGACGGATGGAGATAGAGGCCCTGCCCTGGGCAGCCTCCACCAGGCCAG
TGGCCAGGGGACTTTGCTGAAGAATTAGCAACACTGTCTAATCTGTTTCTAGCCGAGCCCCACCTGCCAGAACCC
CAGCTAAGAGCCTGTGAGTTGGTGCAGCCAAACCGGGGCACTGTGCTGGCCAGAGCTAGGGCTGAGAAGTGGCC
CTGCCCTTGGGCATTGCACCAGAACCCTGGACCCCCGCCTCAGGAGGAGGCCAAGTGCCCAATGCAGACCCTCAC
TGGTTGGGGTGTAGCTGGGTCTACAGTCAGACTTCCCTGCTCTAAGGGTGTCACTGCTGGCATCCCCACACGCGA
ATCCTAGAGGAAGGAGAGTTGGCCTGATTTGGGATTATGGCAGAAAAGTCCAGAGATGCCAGTCTCTGGAGTAGAA
GAGGTGGTGTGTTGTTTATCTCTTGGATACTAAATGAAATGAGGTGTGTGGGCTTGTCACACAGAATTCAAGCCT
CATTGCTATCCCAGCATCTCTTAAACTTTGTAGTCTTGAATTCATGACAGAGGCAATGACTCCTGCTTAAC
TTATGAAGAAGTTAAACATGAATCTTGGGAGTCTACTATTTCTTATCACCAGGAGCTGGACTGCCATCTCCTT
ATAAATGCCCTAACACAGGCCGGGTCTGGTGGCTCATGCTGTAATCCAGCACTTTGAGAGGCCTGAGGTGCGCG
GACTGCCTGAGGTGAGGAATTCAAGACCAGCCTGGCCAACATGGCAAAACCCATCTCTACTAAAAATAAAAAAA
TTATTAGCTGGGCATGGTGGTGTGTGCTGTAATCCAGCTACTCAGGAGGATGAGGCAGGAGACCTGCTTGAAC
CTGGAGGTGGAGGTTCAGTGAGCCGAGGTGCGACCACTGCACTCCAGTCTGGGTAACAGAGCGAGACTTCTAG
AAAAAGCCTAACAAACAGATAAGGTAGGACTCAACCAACTGAAACCTGACTTTCCCCCTGTACCTTCAGCCCTG
TGCAGGTAGTAACCTCTTGAGACCTCTCCCTGACCAGGGACCAAGCACAGGGCATTAGAGCTTTTATAGAATAAA
CTGGTTTTCTTTAAAAAAGGGGCTTTTATTAATTTCTCCCCACAGATGGCTCCTGCAATCTGCCACAGCTC
TGGGGCGTGTCTGTAGGGAAAGGCCCTGTTTCCCTGAGGCGGGCTGGGCTTGTCCATGGGTCCGCGGAGCTG
GCCGTGCTTGGCGCCTGGCGTGTGTCTAGCTGCTTCTTGCCGGGCACAGAGCTGCGGGGTCTGGGGGCACCGGG
AGCTAAGAGCAGGCTCTGGTGCAGGGGTGGAGGCCTGTCTCTTAACCGACACCCTGAGGTGCTCCTGAGATGCTG
GGTCCACCCTGAGTGGCAGCGGGAGCAGCTGTGGCCGGTGTCTCTCYTAGGCCAGTCTGGGGAACTAAGCTC
GGGCCCTTCTTTGCAAAGACCGAGGATGGGGTGGGTGTGGGGGACTCATGGGGAATGGCCTGAGGAGCTACGTG
GAAGAGGGCGCCGGTTTGTGGCTGCAGCGGCTGGAGCGCCTCTCTCCTGAGCCTCAGTTTCCCTTTCCGTCTA
ATGAAGAACATGCCGTCTCGGTGTCTCAGGGCTATTAGGACTTGCCCTCAGGAAGTGGCCTGGACGAGCGTCAT
GTTATTTTCACTGCTGCGACGTTGGCCTGGGCACGTGATGAATGGCCCATGTCCCTCTGCTGCGTGGAC
GTCGCGGTGCGGAGTGCGCAGCCAGAGGCGGGGCCAGACGTGCGCCTGGGGGTGAGGGGAGGCGCCCGGGAGGG
CCTCACAGGAAGTTGGGCTCCCGCACCCAGGCAGGGCGGGCTCCCGCCGCGCGCCGCCACACCGTCCAGG
GGCCGGTAGACAAAGTGAAGTCGCGCTTGGGCTGCTGCGCAGCAGGTAGCCCTTGATGAGTGCAGGAGCGCG
TCGTCCGCCAGCTGGAAGCAGCGCCCGTCCACCAGCACGAACAGCCGGTGCAGCT

FIGURE 32

MCFLNKLLLLAVLGWLFQIPTVPEDLFFLEEGPSYAFEVDTVAPEHGLDNAPVVDQQLLYTC
CPYIGELRKLLASWVSGSSGRSGGFMRKITPTTTTSLGAQPSQTSQGLQAQLAQAFFHNQPP
SLRRTVEFVAERIGSNCVKHIKATLVADLVRQAESLLQEQLVTQGEEGDPAQLLEILCSQL
CPHGAQALALGREFCQRKSPGAVRALLPEETPAAVLSSAENIAVGLATEKACAWLSANITAL
IRREVKAAVSRTLRAQGPEPAARGERRGCSRA

Signal peptide:

amino acids 1-18

N-glycosylation site.

amino acids 244-248

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 89-93

Casein kinase II phosphorylation site.

amino acids 21-25, 167-171, 223-227

N-myristoylation site.

amino acids 100-106, 172-178, 207-213

Microbodies C-terminal targeting signal.

amino acids 278-282

FIGURE 33

TCCCTTGACAGGTCTGGTGGCTGGTTCGGGGTCTACTGAAGGCTGTCTTGATCAGGAACTG
AAGACTCTCTGCTTTTGCCACAGCAGTTCTTGCAGCTTCCTTGAGGTGTGAACCCACATCCC
TGCCCCCAGGGCCACCTGCAGGACGCCGACACCTACCCCTCAGCAGACGCCGGAGAGAAATG
AGTAGCAACAAAGAGCAGCGGTGAGCAGTGTTCGTGATCCTCTTTGCCCTCATCACCATCCT
CATCCTCTACAGCTCCAACAGTGCCAATGAGGTCTTCCATTACGGCTCCCTGCGGGGCCGTA
GCCGCCGACCTGTCAACCTCAAGAAGTGGAGCATCACTGACGGCTATGTCCCCATTCTCGGC
AACAAGACACTGCCCTCTCGGTGCCACCAGTGTGTGATTGTGAGCAGCTCCAGCCACCTGCT
GGGCACCAAGCTGGGCCCTGAGATCGAGCGGGCTGAGTGTACAATCCGCATGAATGATGCAC
CCACCACTGGCTACTCAGCTGATGTGGGCAACAAGACCACCTACCGCGTCGTGGCCCCATTCC
AGTGTGTTCCGCGTGTCTGAGGAGGCCCCAGGAGTTTGTCAACCGGACCCCTGAAACCGTGT
CATCTTCTGGGGGCCCCCGAGCAAGATGCAGAAGCCCCAGGGCAGCCTCGTGCGTGTGATCC
AGCGAGCGGGCCTGGTGTTCCTCAACATGGAAGCATATGCCGTCTCTCCCGGCCGCATGCGG
CAATTTGACGACCTCTTCCGGGGTGAGACGGGCAAGGACAGGGAGAAGTCTCATTCGTGGTT
GAGCACAGGCTGGTTTACCATGGTGATCGCGGTGGAGTTGTGTGACCAGTGCATGTCTATG
GCATGGTCCCCCCCCAACTACTGCAGCCAGCGGCCCCCGCTCCAGCGCATGCCCTACCACTAC
TACGAGCCCAAGGGGCCGACGAATGTGTACCTACATCCAGAATGAGCACAGTCGCAAGGG
CAACCACCACCGCTTCATCACCAGAGAAAAGGGTCTTCTCATCGTGGGCCCAGCTGTATGGCA
TCACCTTCTCCCACCCCTCCTGGACCTAGGCCACCCAGCCTGTGGGACCTCAGGAGGGTCAG
AGGAGAAGCAGCCTCCGCCCAGCCGCTAGGCCAGGGACCATCTTCTGGCCAATCAAGGCTTG
CTGGAGTGTCTCCAGCCAATCAGGGCCTTGAGGAGGATGTATCCTCCAGCCAATCAGGGCC
TGGGGAATCTGTTGGCGAATCAGGGATTTGGGAGTCTATGTGGTTAATCAGGGGTGTCTTTC
TTGTGCAGTCAGGGTCTGCGCACAGTCAATCAGGGTAGAGGGGGTATTTCTGAGTCAATCTG
AGGCTAAGGACATGTCCTTTCCCATGAGGCCTTGGTTCAGAGCCCCAGGAATGGACCCCCCA
ATCACTCCCCACTCTGCTGGGATAATGGGGTCTGTCCCAAGGAGCTGGGAACTTGGTGTG
CCCCCTCAATTTCCAGCACCAGAAAAGAGAGATTGTGTGGGGGTAGAAGCTGTCTGGAGGCCC
GGCCAGAGAATTTGTGGGGTGTGGAGGTTGTGGGGGCGGTGGGGAGGTCCCAGAGGTGGGA
GGCTGGCATCCAGGTCTTGGCTCTGCCCTGAGACCTTGGACAAACCCTTCCCCCTCTCTGGG
CACCTTCTGCCCCACACCAGTTTCCAGTGCAGGAGTCTGAGACCCTTCCACCTCCCCTACAA
GTGCCCTCGGGTCTGTCTCCCCGTCTGGACCTCCCAGCCACTATCCCTTGCTGGAAGGCT
CAGCTCTTTGGGGGGTCTGGGGTGACCTCCCCACCTCCTGGAAAACCTTTAGGGTATTTTTC
GCAAACCTCCTTCAGGGTTGGGGGACTCTGAAGGAAACGGGACAAAACCTTAAGCTGTTTTCT
TAGCCCCCTCAGCCAGCTGCCATTAGCTTGGCTCTTAAAGGGCCAGGCCTCCTTTTCTGCCCT
CTAGCAGGGAGGTTTTTCCAACGTGTTGGAGGCGCCTTTGGGGCTGCCCTTTGTCTGGAGTCA
CTGGGGGCTTCCGAGGGTCTCCCTCGACCCTCTGTCTCTGGGATGGCTGTGCGGAGCTGT
ATCACCTGGGTTCTGTCCCCTGGCTCTGTATCAGGCACTTTATTAAAGCTGGGCCTCAGTGG
GGTGTGTTTGTCTCCTGCTCTTCTGGAGCCTGGAAGGAAAGGGCTTCAGGAGGAGGCTGTGA
GGCTGGAGGGACCAGATGGAGGAGGCCAGCAGCTAGCCATTGCACACTGGGGTGATGGGTGG
GGGCGGTGACTGCCCCAGACTTGGTTTTGTAAATGATTTGTACAGGAATAAACACACCTACGC
TCCGGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 34

MSSNKEQRSAVFVILFALITILILYSSNSANEVFHYGSLRGRSRRPVNLKKWSITDGYVPIL
GNKTLPSRCHQCIVIVSSSSHLLGTLGPEIERAECTIRMNDAPTTGYSADVGNKTTYRVVAH
SSVFRVLRRPQEFVNRTPETVFIFWGPPSKMQKPQGSLVRVIQRAGLVFPNMEAYAVSPGRM
RQFDDLFRGETGKDREKSHSWLSTGWFTMVI AVELCDHVHVYGMVPPNYCSQRPRLQRMPYH
YYEPKGPDECVTYIQNEHSRKGNHHRFITEKRVFSSWAQLYGITFSHPSWT

Signal peptide:

amino acids 1-29

Transmembrane domain:

amino acids 9-31 (type II)

N-glycosylation site.

amino acids 64-68, 115-119

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 50-54

Casein kinase II phosphorylation site.

amino acids 3-7, 29-33, 53-57, 197-201

Tyrosine kinase phosphorylation site.

amino acids 253-262

N-myristoylation site.

amino acids 37-43, 114-120, 290-294

FIGURE 35

GTTCCTCATAGTTGGCGTCTTCTAAAGGAAAAACACTAAAATGAGGAACTCAGCGGACCGGGAGCGACGCAGCTT
GAGGGAAGCATCCCTAGCTGTTGGCGCAGAGGGGCGAGGCTGAAGCCGAGTGGCCCCAGGTGTCTGAGGGGCTGG
GGCAAAGGTGAAAGAGTTTCAGAAACAAGCTTCTTGAACCCATGACCCATGAAGTCTTGTGACATTATACCGT
CTGAGGGTAGCAGCTCGAACTAGAAGAAGTGGAGTGTGCCAGGGACGGCAGTATCTCTTTGTGTGACCCTGGC
GGCCTATGGGACGTTGGCTTCAGACCTTTGTGATACACCATGCTGCGTGGGACGATGACGGCGTGGAGAGGAATG
AGGCCTGAGGTACACTGGCTTGCTCCTCTAGCCACAGCAGGCTGCTTTGCTGACTTGAACGAGGTCCCTCAG
GTCACCGTCCAGCTGCGTCCACCGTCCAGAAGCCCGAGGCACTGTGATCTTGGGCTGCGTGGTGGAACTCCA
AGGATGAATGTAACCTGGCGCTGAATGGAAAGGAGCTGAATGGCTCGGATGATGCTCTGGGTGTCTCATCACC
CACGGGACCTCGTCATCACTGCCCTTAACAACCACACTGTGGGACGGTACCAGTGTGTGGCCCGGATGCTGCG
GGGGCTGTGGCCAGCGTCCAGCCACTGTGACACTAGCCAATCTCCAGGACTTCAAGTTAGATGTGCAGCACGTG
ATTGAAGTGGATGAGGGAAACACAGCAGTCATTGCTGCCACCTGCCCTGAGAGCCACCCCAAAGCCAGGTCCGG
TACAGCGTCAAACAAGAGTGGCTGGAGGCCTCCAGAGGTAACCTACCTGATCATGCCCTCAGGGAACCTCCAGATT
GTGAATGCCAGCCAGGAGGACGAGGGCATGTACAAGTGTGCAGCCCTACAACCCAGTGACCCAGGAAGTGAACAC
TCCGGCTCCAGCGACAGGCTACGTGTGCGCCGCTCCACCGCTGAGGCTGCCCCGATCATCTACCCCCCAGAGGCC
CAAACCATCATCGTCACCAAAGGCCAGAGTCTATTCTGGAGTGTGTGGCCAGTGAATCCCACCCCCACGGGTC
ACCTGGGCCAAGGATGGGTCCAGTGTACCCGGCTACAACAAGACGCGCTTCTGCTGAGCAACCTCCTCATCGAC
ACCACCAGCGAGGAGGACTCAGGCACCTACCGCTGCATGGCCGACAATGGGGTTGGGCAGCCCGGGGACGCGGTC
ATCCTCTACAATGTCCAGGTGTTTGAACCCCCCTGAGGTCACTATGGAGCTATCCAGCTGGTTCATCCCCTGGGGC
CAGAGTGCCAAAGCTTACCTGTGAGGTGCGTGGGAACCCCCGCCCTCGTGCTGTGCTGGTGGTGTCTGCCCC
CTCATCTCCAGCCAGCGCCTCCGGCTCTCCCGCAGGGCCCTGCGCGTGCTCAGCATGGGGCTGAGGACGAAGGC
GTCTACCAGTGCATGGCCGAGAACGAGGTTGGGAGCGCCCATGCCGTAGTCCAGCTGCGGACCTCCAGGCCAAGC
ATAACCCCAAGGCTATGGCAGGATGCTGAGCTGGCTACTGGCACACCTCCTGTATCACCTCCAAACTCGGCAAC
CCTGAGCAGATGCTGAGGGGGCAACCGGCGCTCCCCAGACCCCCAACGTCAGTGGGGCTGCTTCCCCGAAGTGT
CCAGGAGAGAAGGGGACGGGGGCTCCCGCCGAGGCTCCATCATCTCAGCTCGCCCCGACCTCCAAGACAGAC
TCATATGAAGTGGTGTGGCGGCCTCGGCATGAGGGCAGTGGCCGGGCGCAATCCTCTACTATGTGGTGAACAC
CGCAAGCAGGTACAAATTCTCTGACGATTGGACCATCTCTGGCATTCAGCCAACAGCACCGCCTGACCCCTC
ACCAGACTTGACCCCGGGAGCTTGTATGAAGTGGAGATGGCAGCTTACAAGTGTGCGGGAGAGGGCCAGACAGCC
ATGGTCACCTTCCGAACCTGGACGGCGGCCCAAACCCGAGATCATGGCCAGCAAGAGCAGCAGATCCAGAGAGAC
GACCCTGGAGCCAGTCCCCAGAGCAGCAGCCAGCCAGACACCGCCGCTCTCCCCCAGAAGCTCCCGACAGG
CCCACCATCTCCACGGCCTCCGAGACCTCAGTGTACGTGACCTGGATTCCCGCTGGGAATGGTGGTGTCCCAATC
CAGTCTCTCCGTGTGGAGTACAAGAAGCTAAAGAAAGTGGGAGACTGGATTCTGGCCACCAGCGCCATCCCCCA
TCGCGGCTGTCCGTGGAGATCACGGGCTAGAGAAAGGCACCTCCTACAAGTTTCGAGTCCGGGCTCTGAACATG
CTGGGGGAGAGCGAGCCCAGCGCCCCCTCTCGGCCCTACGTGGTGTGCGGGCTACAGCGGTGCGGTGTACGAGAGG
CCCGTGGCAGGTCTTATATCACCTTACGGATGCGGTCAATGAGACCACCATCATGCTCAAGTGGATGTACATC
CCAGCAAGTAACAACAACACCCCAATCCATGGCTTTTATATCTATTATCGACCCACAGACGATGACATGATG
GACTACAAGAAGGATATGGTGAAGGGGACAAAGTGGGACTCCATCAGCCACCTGACGCCAGAGACCTCCTAC
GACATTAAGATGCAGTGCTTCAATGAAGGAGGGGAGAGCGAGTTTCAGCAACGTGATGATCTGTGAGACCAAGCT
CGGAAGTCTTCTGGCCAGCCTGGTTCGACTGCCACCCCCAAGCTCTGGCCCCACCACAGCCGCCCCCTTCTGAAACC
ATAGAGCGGCCGGTGGGCACTGGGGCCATGGTGGCTCGCTCCAGCGACCTGCCCTATCTGATTGTGCGGGTCTGTC
CTGGGCTCCATCGTTCTCATCATCGTCACCTTCATCCCCCTTCTGCTTGTGGAGGGCCTGGTCTAAGCAAAAACAT
ACAACAGACCTGGGTTTTCTCGAAGTGCCCTTCCACCTCCTGCCCCGATATGTTGGTGGCATTGGGAGGACTC
CCAGGCCACCAGGCCAGTGGACAGCCCTACCTCAGTGGCATCAGTGGACGGGCTGTGCTAATGGGATCCACATG
AATAGGGGCTGCCCCCTCGGCTGCAGTGGGCTACCCGGGCATGAAGCCCAGCAGCACTGCCAGGCGAGCTTCAG
CAGCAGAGTGACACCAGCAGCCTGCTGAGGCAGACCCATCTTGGCAATGGATATGACCCCCAAAGTCAACAGATC
ACGAGGGGTCCCAAGTCTAGCCCGGACGAGGGCTCTTCTTATACACACTGCCCGACGACTCCACTCACCAGCTG
CTGCAGCCCCATCACGACTGCTGCCAACGCCAGGAGCAGCCTGCTGCTGTGGGCCAGTCAGGGGTGAGGAGAGCC
CCCGACAGTCTCTGCTGGAAGCAGTGTGGGACCTCCATTTCACTCAGGGCCCCATGCTGCTTGGGCTTGTG
CCAGTTGAAGAGGTGGACAGTCTGACTCCTGCCAAGTGAGTGGAGGAGACTGGTGTCCCCAGCACCCTGAGGG
GCCTACGTAGGACAGGAACCTGGAATGCAGCTCTCCCGGGGCCACTGGTGGTGTGTCTTTGAAACACCACCT
CTCACAATTTAGGCAGAGCTGATATCCAGAAAGACTATATATTGTTTTTTTTTAAAAAAGAAAGAAAA
AGAGACAGAGAAAAATTGGTATTTATTTTCTATTATAGCCATATTTATATATTTATGCACTTGTAAATAAATGTA
TATGTTTTATAATTCTGGAGAGACATAAGGAGTCTTACCCGTGAGGTTGGAGAGGAAAAATAAGAAGCTGCCA
CCTAACAGGAGTCAACCCAGGAAAGCACCGCACAGGCTGGCGGGACAGACTCCTAACCTGGGGCTCTGCAGTG
GCAGGCGAGGCTGCAGGAGGCCCCACAGATAAGCTGGCAAGAGGAAGGATCCAGGCACATGGTTCATCAGGACA
TGAGGGAACAGCAAGGGGACGGTATCACAGCCTGGAGACACCCACAGATGGCTGGATCCGGTGTACGGGAA
ACATTTCTCTAAGATGCCCATGAGAACAGACCAAGATGTGTACAGCACTATGAGCATTAACCACTTCCAGAA
CAATAATCCGTGGCAACATATCTCTGTAAAAACAACACTGTAACCTCTAAATAAATGTTTAGTCTTCCCTGTAAAA

FIGURE 36

MLRGTMTAWRGMREVTLACLLLATAGCFADLNEVPQVTVQPASTVQKPGGTIVLGCVVEPP
RMNVTWRLNGKELNGSDDALGVLI THGTLVITALNNHTVGRYQCVARMPAGAVASVPATVTL
ANLQDFKLDVQHVIEVDEGNTAVIACHLPESHKPAQVRYSVKQEWLEASRGNYLIMPSGNLQ
IVNASQEDEGMYKCAAYNPVTQEVKTSGSSDRLRVRRSTAEAAARI IYPPAQTI IVTKGQSL
ILECVASGIPPPRVTWAKDGSSVTGYNKTRFLLSNLLIDTTSEEDSGTYRCMADNGVGQPGA
AVILYNVQVFEPPEVTMELSQLVIPWGQSAKLTCEVRGNPPPSVLWLRNAVPLISSQRLRLS
RRALRVLSMGPEDGVEYQCMANEVGSAAHVQLRTSRPSITPRLWQDAELATGTPPVSPSK
LGNPEQMLRGQPALPRPPTSVGPASPKCPGEGKQGAPAEAPIILSSPRTSKTDSYELVWRPR
HEGSGRAPILYYVVKHRKQVTNSSDDWTISGIPANQHRLTLTRLDPGSLYEVEMAAYNCAGE
GQTAMVTFRTGRRPKPEIMASKEQQIQRDDPGASQSSSQPDHGRLSPPEAPDRPTISTASE
TSVYVTWI PRNGGFPIQSFRVEYKKLKKVGDWILATSAIPPSRLSVEITGLEKGT SYKFRV
RALNMLGESEPSAPSRPYVVS GYSGRVYERPVAGPYITFTDAVNETTIMLKWMI PASNNNT
PIHGFYIYRPTDSDNDSYK KDMVEGDKYWHSISHLQ PETS YDIKMQCFNEGGESEFSNVM
ICETKARKSSGQPGR LPPPTLAPPQPPLPETIERPVGTGAMVARSSDLPYLIVGVVLGSIVL
IIVTFIPFCLWRAW SKQKHTTDLGFPR SALPPSCPYTMVPLGGLPGHQASGQPYLSGISGRA
CANGIHMNRGCP SAAVGYPGMKPQQHCPGELQQQSDTSSLLRQTHLGNGYDPQSHQITRGPK
SSPDEGSFLYTL PDDSTHQLLQPHHDCCQRQE QPAAVGQSGVRRAPDSPVLEAVWDP PFHSG
PPCCLGLVPVEEVDSPDSCQVSGGDWCPQHPVGAYVGQEPGMQLSPGPLVRVSFETPPLTI

Signal peptide:

amino acids 1-30

Transmembrane domain:

amino acids 16-30 (type II), 854-879

FIGURE 37

CGGGAGGCTGGGTCGTCATGATCCGGACCCCATTTGTGGCCTCTGCCCATCGCCTGCTCCTC
CCAGGCTCCCGCGGCCGACCCCGCGCAACATGCAGCCCACGGGCCGCGAGGGTTCCCGCGC
GCTCAGCCGGCGGTATCTGCGGCGTCTGCTGCTCCTGCTACTGCTGCTGCTGCTGCGGCAGC
CCGTAACCCGCGCGGAGACCACGCCGGGCGCCCCAGAGCCCTCTCCACGCTGGGCTCCCC
AGCCTCTTACCACGCCGGGTGTCCCCAGCGCCCTCACTACCCAGGCCTCACTACGCCAGG
CACCCCCAAAACCCTGGACCTTCGGGGTTCGCGCGCAGGCCCTGATGCGGAGTTTCCCACTCG
TGGACGGCCACAATGACCTGCCCCAGGTCCTGAGACAGCGTTACAAGAATGTGCTTCAGGAT
GTTAACCTGCGAAATTTAGCCATGGTACAGCCAGCCTGGACAGGCTTAGAGACGGCCTCGT
GGGTGCCCAGTTCTGGTCAGCCTCCGTCTCATGCCAGTCCCAGGACCAGACTGCCGTGCGCC
TCGCCCTGGAGCAGATTGACCTCATTACCGCATGTGTGCCTCCTACTCTGAACCTCGAGCTT
GTGACCTCAGCTGAAGGTCTGAACAGCTCTCAAAGCTGGCCTGCCTCATTGGCGTGNAGGG
TGGTCACTCACTGGACAGCAGCCTCTCTGTGCTGCGCAGTTTCTATGTGCTGGGGGTGCGCT
ACCTGACACTTACCTTACCTGCAGTACACCATGGGCAGAGAGTTCACCAAGTTCAGACAC
CACATGTACACCAACGTCAGCGGATTGACAAGCTTTGGTGAGAAAGTAGTAGAGGAGTTGAA
CCGCCTGGGCATGATGATAGATTTGTCTATGCATCGGACACCTTGATAAGAAGGGTCTCGG
AAGTGTCTCAGGCTCCTGTGATCTTCTCCCACTCAGCTGCCAGAGCTGTGTGTGACAATTTG
TTGAATGTTCCCGATGATATCCTGCAGCTTCTGAAGAACGGTGGCATCGTGATGGTGACACT
GTCCATGGGGGTGCTGCAGTGC AACCTGCTTGCTAACGTGTCCACTGTGGCAGATCACTTTG
ACCACATCAGGGCAGTCATTGGATCTGAGTTCATCGGGATTGGTGGAATTATGACGGGACT
GGCCGGTTCCCTCAGGGGCTGGAGGATGTGTCCACATACCCAGTCCTGATAGAGGAGTTGCT
GAGTCGTASCTGGAGCGAGGAAGAGCTTCAAGGTGTCCTTCGTGGAAACCTGCTGCGGGTCT
TCAGACAAGTGGAAGGTGAGAGAGGAGAGCAGGGCGCAGAGCCCCGTGGAGGCTGAGTTT
CCATATGGGCAACTGAGCACATCCTGCCACTCCCACCTCGTGCCTCAGAATGGACACCAGGC
TACTCATCTGGAGGTGACCAAGCAGCCAACCAATCGGGTCCCCTGGAGGTCTCAAATGCCT
CCCCATACCTTGTTCCAGGCCTTGTGGCTGCTGCCACCATCCCAACCTTACCCAGTGGCTC
TGCTGAACACAGTCGGTCCCCGCGAGAGGTCACTGTGGCAAAGCCTCACAAAGCCCCCTCTCCT
AGTTCATTACAAGCATATGCTGAGAATAAACATGTTACACATGGAAAA

FIGURE 38

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA59817

><subunit 1 of 1, 487 aa, 1 stop, 2 unknown

><MW: 53569.32, pI: 7.68, NX(S/T): 5

MQPTGREGSRALSRRLRLRLRLRLRLRLRLRLRQPVTRAETTPGAPRALSTLGSPSLFTTPGVPS
ALTTPGLTTPGTPKTLDLRGRAQALMRSFPLVDGHNDLPQVLRQRYKNVLQDVNLRNFSGHQ
TSLDRLRDGLVGAQFWSASVSCQSQDQTAVRLALEQIDLIHRMCASYSELELVTSAEGLNSS
QKLACLIGVXGGHSLDSSLSVLRSFYVLGVRYLTLTFTCSTPWAESSTKFRHHMYTNVSGLT
SFGEKVVEELNRLGMMIDLSYASDTLIRRVLEVSQAPVIFSHSAARAVCDNLLNVPDDILQL
LKNGGIVMVTLSMGVLQCNLLANVSTVADHFDHIRAVIGSEFIGIGGNYDGTGRFPQGLEDV
STYPVLIEELLSRXWSEEELQGVLRGNLLRVFRQVEKVREESRAQSPVEAEFPYQQLSTSCH
SHLVPQNGHQATHLEVTKQPTNRVPWRSSNASPYLVPGLVAAATIPTFTQWLC

Important features of the protein:

Signal peptide:

amino acids 1-36

Transmembrane domain:

amino acids 313-331

N-glycosylation sites.

amino acids 119-122, 184-187, 243-246 and 333-336

N-myristoylation sites.

amino acids 41-46, 59-64, 73-78, 133-138, 182-187, 194-199, 324-329, 354-359, 357-362, 394-399, 427-432 and 472-477.

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 136-146

FIGURE 39

TGCTAGGCTCTGTCCCACAATGCACCCGAGAGCAGGAGCTGAAAGCCTCTAACACCCACAGA
TCCCTCTATGACTGCAATGTGAGGTGTCCGGCTTTGCTGGCCCAGCAAGCCTGATAAGCATG
AAGCTCTTATCTTTGGTGGCTGTGGTCGGGTGTTTGCTGGTGCCCCAGCTGAAGCCAACAA
GAGTTCTGAAGATATCCGGTGCAAATGCATCTGTCCACCTTATAGAAACATCAGTGGGCACA
TTTACAACCAGAATGTATCCCAGAAGGACTGCAACTGCCTGCACGTGGTGGAGCCCATGCCA
GTGCCTGGCCATGACGTGGAGGCCTACTGCCTGCTGTGCGAGTGCAGGTACGAGGAGCGCAG
CACCACCACCATCAAGGTCATCATTGTCATCTACCTGTCCGTGGTGGGTGCCCTGTTGCTCT
ACATGGCCTTCCTGATGCTGGTGGACCCTCTGATCCGAAAGCCGGATGCATACACTGAGCAA
CTGCACAATGAGGAGGAGAATGAGGATGCTCGCTCTATGGCAGCAGCTGCTGCATCCCTCGG
GGGACCCCGAGCAAACACAGTCCTGGAGCGTGTGGAAGGTGCCCAGCAGCGGTGGAAGCTGC
AGGTGCAGGAGCAGCGGAAGACAGTCTTCGATCGGCACAAGATGCTCAGCTAGATGGGCTGG
TGTGGTTGGGTCAAGGCCCAACACCATGGCTGCCAGCTTCCAGGCTGGACAAAGCAGGGGG
CTACTTCTCCCTTCCCTCGGTTCCAGTCTTCCCTTTAAAAGCCTGTGGCATTTTTCCCTCCTT
CTCCCTAACTTTAGAAATGTTGTACTTGGCTATTTTGATTAGGGAAGAGGGATGTGGTCTCT
GATCTCTGTTGTCTTCTTGGGTCTTTGGGGTTGAAGGGAGGGGAAGGCAGGCCAGAAGGGA
ATGGAGACATTTCAGGCGGCCTCAGGAGTGGATGCGATCTGTCTCTCCTGGCTCCACTCTTG
CCGCCTTCCAGCTCTGAGTCTTGGGAATGTTGTTACCCTTGAAGATAAAGCTGGGTCTTCA
GGAAGTCAAGTGTCTGGGAGGAAAGCATGGCCAGCATTAGCATGTGTTCTTTCTGCAGTG
GTTCTTATCACCACCTCCCTCCCAGCCCCGGCGCCTCAGCCCCAGCCCCAGCTCCAGCCCTG
AGGACAGCTCTGATGGGAGAGCTGGGCCCCCTGAGCCCACTGGGTCTTCAGGGTGCACCTGGA
AGCTGGTGTTCGCTGTCCCCTGTGCACTTCTCGCACTGGGGCATGGAGTGCCCATGCATACT
CTGCTGCCGGTCCCCTCACCTGCACTTGAGGGGTCTGGGCAGTCCCTCCTCTCCCCAGTGTC
CACAGTCACTGAGCCAGACGGTCGGTTGGAACATGAGACTCGAGGCTGAGCGTGGATCTGAA
CACCACAGCCCCGTGACTTGGGTGCTCTTGTCCCTGAACTTCGTTGTACCAGTGCATGGA
GAGAAAATTTTGTCTCTTGTCTTAGAGTTGTGTGTAATCAAGGAAGCCATCATTAATTG
TTTTATTCTCTCA

FIGURE 40

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA60278

<subunit 1 of 1, 183 aa, 1 stop

<MW: 20574, pI: 6.60, NX(S/T): 3

MKLLSLVAVVGCLLVPPAEANKSSEDIRCKCICPPYRNISGHIYNQNVSQKDCNCLHVVEPM
PVPGH DVEAYCLLCECRYEERSTTTIKVIIIVYLSVVGALLLYMAFLMLVDPLIRKPDAYTE
QLHNEEENEDARSMAAAAASLGGPRANTVLERVEGAQQRWKLQVQEQRKTVFDRHKMLS

Important features:**Signal peptide:**

amino acids 1-20

Transmembrane domain:

amino acids 90-112

N-glycosylation sites.

amino acids 21-24, 38-41 and 47-50

40/270

FIGURE 41

AGCGGGTCTCGCTTGGGTTCCGCTAATTTCTGTCTGAGGCGTGAGACTGAGTTTCATAGGGTCTGGGTCCCCGA
ACCAGGAAGGGTTGAGGGAACACAATCTGCAAGCCCCGCGACCCAAGTGAGGGGCCCCGTGTTGGGGTCTCCC
TCCCTTTGCAATCCCAACCCCTCCGGGCTTTGCGTCTTCTGGGGACCCCTCGCCGGGAGATGGCCGCTTGATG
CGGAGCAAGGATTCGTCTGTGCTGCTCTACTGGCCGCGGTGCTGATGGTGGAGAGCTCACAGATCGGCAGT
TCGCGGGCCAACTCAACTCCATCAAGTCTCTCTGGGCGGGGAGACGCTGGTCAGGCCGCCAATCGATCTGCG
GGCATGTACCAAGGACTGGCATTGGCGGCAGTAAGAAGGGCAAAAACCTGGGGCAGGCCTACCCTGTAGCAGT
GATAAGGAGTGTGAAGTTGGGAGGTATTGCCACAGTCCCCACCAAGGATCATCGGCCTGCATGGTGTGTCGGAGA
AAAAAGAAGCGCTGCCACCGAGATGGCATGTGTGCCCCAGTACCCGCTGCAATAATGGCATCTGTATCCCAGTT
ACTGAAAGCATCTTAACCCCTCACATCCCGGCTCTGGATGGTACTCGGCACAGAGATCGAAACCACGGTCATTAC
TCAAACCATGACTTGGGATGGCAGAATCTAGGAAGACCACACACTAAGATGTCACATATAAAGGGCATGAAGGA
GACCCCTGCCTACGATCATCAGACTGCATTGAAGGGTTTTGCTGTGCTCGTCATTTCTGGACCAAAATCTGCAAA
CCAGTGCTCCATCAGGGGGAAGTCTGTACCAACAACGCAAGGAGGTTCTCATGGGCTGGAAATTTCCAGCGCT
TGCGACTGTGCGAAGGGCCTGTCTTGCAAGATATGAAAGATGCCACCTACTCCTCCAAAGCCAGACTCCATGTG
TGTCAGAAAATTTGATCACCATTGAGGAACATCATCAATTGCAGACTGTGAAGTTGTGTATTTAATGCATTATAG
CATGGTGGAAAATAAGGTTTCAGATGCAGAAGAATGGCTAAAATAAGAAACGTGATAAGAATATAGATGATCAGAA
AAAGGGAGAAAGAAAACATGAAGTGAATAGATTAGAATGGGTGACAAATGCAGTGCAGCCAGTGTTCATTATG
CAACTTGTCTATGTAATAATGTACACATTTGTGGAAAATGCTATTATTAAGAGAACAAGCACACAGTGGAAAT
ACTGATGAGTAGCATGTGACTTTCCAAGAGTTTAGGTTGTGCTGGAGGAGAGGTTTCTTCAGATTGCTGATTGC
TTATACAAATAACCTACATGCCAGATTTCTATTCAACGTTAGAGTTTAAACAAATACTCCTAGAATAACTTGTTA
TACAATAGGTTCTAAAAATAAAATGCTAAACAAGAAATGAAACATGGAGCATTGTTAATTTACAACAGAAAAT
TACCTTTTGATTTGTAACACTACTTCTGCTGTTCAATCAAGAGTCTTGGTAGATAAGAAAAAATCAGTCAATAT
TTCCAAATAAATGCAAAATAATGGCCAGTTGTTTAGGAAGGCCCTTAGGAAGACAAATAAATAACAAACAAACAG
CCACAAATACTTTTTTTTCAAATTTTAGTTTTACCTGTAATTAATAAGAACTGATACAAGACAAAAACAGTTC
TTCAGATTCTACGGAATGACAGTATATCTCTTTATCTATGTGATTCTGTCTGTAATGCATTATATTTTCCA
AACTATACCCATAAATTGTGACTAGTAAAATACCTACACAGAGCAGAATTTTCACAGATGGCAAAAAATTTAA
GATGTCCAATATATGTGGGAAAAGAGCTAACAGAGAGATCATTATTTCTTAAAGATTGGCCATAACCTATATTT
GATAGAATTAGATTGGTAAATACATGTATTCATACATACTCTGTGGTAATAGAGACTTAAGCTGGATCTGTACTG
CACTGGAGTAAGCAAGAAAATTTGGGAAAACCTTTTCGTTTGTTCAGGTTTTGGCAACACATAGATCATATGTCTG
AGGCACAAGTTGGCTGTTTCATCTTTGAAACCAGGGGATGCACAGTCTAAATGAATATCTGCATGGGATTGCTAT
CATAATATTTACTATGCAGATGAATTCAGTGTGAGGTCTGTGTCCGTACTATCCTCAAATTATTTATTTATAG
TGCTGAGATCCTCAAATAATCTCAATTTTCAGGAGGTTTCACAAAATGTACTCCTGAAGTAGACAGAGTAGTGAGG
TTTCATTGCCCTCTATAAGCTTCTGACTAGCCAATGGCATCATCCAATTTTCTCCCAACCTCTGCAGCATCTG
CTTTATTGCCAAAGGGCTAGTTTCGGTTTTCTGCAGCCATTGCGGTTAAAAAATATAAGTAGGATAACTTGTA
ACCTGCATATTGCTAATCTATAGACACCACAGTTTCTAAATTTCTTGAAACCCTTTACTACTTTTTTTAACTT
AACTCAGTTCTAAATACTTTGTCTGGAGCACAAAACAATAAAAGGTTATCTTATAGTCGTGACTTTAACTTTTG
TAGACCACAATTCATTTTGTAGTTTTCTTTACTTAAATCCCATCTGCAGTCTCAAATTTAAGTTCTCCCAGTAG
AGATTGAGTTTGAGCCTGTATATCTATTAATAATTTCAACTTCCCACATATATTTACTAAGATGATTAAGACTTA
CATTTTCTGCACAGGTCTGCAAAAACAAAATTTATAAACTAGTCCATCCAAGAACCAGGTTTGTATAACAGGT
TGCTATAAGCTTGTGAAATGAAATGGAACATTTCAATCAAAACATTTCTATATAACAATTATTATTTACAAT
TTGGTTTCTGCAATATTTTCTTATGTCCACCTTTTAAAGATTATTTTGAAGTAATTTATTTACAGGAAATG
TTAATGAGATGTATTTCTTATAGAGATATTTCTTACAGAAAGCTTTGTAGCAGAATATATTTGCAGCTATTGAC
TTTGTAAATTTAGGAAAAATGTATAATAAGATAAAATCTATTAAATTTTCTCCTCTAAAAACTGAAAAA
AAAAAAAAAAAAAAAAAAAA

FIGURE 42

MAALMRSKDSSCCLLLLLAAVLMVESSQIGSSRAKLNSIKSSLGGETPGQAANRSAGMYQGLA
FGGSKKGKNLGQAYPCSSDKECEVGRYCHSPHQSSACMVCRRKKKRCHRDGMCCPSTRCNN
GICIPVTESILTPHIPALDGTRHRDRNHGHYSNHDLGWQNLGRPHTKMSHIKGHEGDPCLRS
SDCIEGFCCARHFWTKICKPVLHQGEVCTKQRKKGSHGLEIFQRCDCAKGLSCKVWKDATYS
SKARLHVCQKI

Signal peptide:

amino acids 1-25

FIGURE 43

TCTCAATCTGCTGACCTCGTGATCCGCCTGACCTTGTAATCCACCTACCTTGGCCTCCCAA
GTGTTGGGATTACAGGCGTGAGCCACCGCGCCCGGCCAACATCACGTTTTTAAAAATTGATT
TCTTCAAATTCATGGCAAATATTTCCCTTCCCTTTAACTTCTTATGTCAGAATGAGGAAGGA
TAGCTGCATTTATTTAGTCAGTTTTTCATTGCATAGTAATATTTTCATGTAGTATTTTCTAAG
TTATATTTTAGTAATTCATATGTTTTAGATTATAGGTTTTAACATACTTGTGAAAATACTTG
ATGTGTTTTAAAGCCTTGGGCAGAAATTCTGTATTGTTGAGGATTTGTTCTTTTATCCCCCT
TTTAAAGTCATCCGTCCTTGGCTCAGGATTTGGAGAGCTTGCACCACCAAAATGGCAAACA
TCACCAGCTCCCAGATTTTGGACCAGTTGAAAGCTCCGAGTTTGGGCCAGTTTACCACCACC
CCAAGTACACAGCAGAATAGTACAAGTCACCCTACAACCTACTACTTCTTGGGACCTCAAGCC
CCCAACATCCCAGTCCTCAGTCCTCAGTCATCTTGACTTCAAATCTCAACCTGAGCCATCCC
CAGTTCCTTAGCCAGTTGAGCCAGCGACAACAGCACCAGAGCCAGGCAGTCACTGTTCCCTCCT
CCTGGTTTTGGAGTCCTTTCTTCCCAGGCAAACTTCGAGAATCAACACCTGGAGACAGTCC
CTCCACTGTGAACAAGCTTTTGCAGCTTCCCAGCACGACCATTGAAAATATCTCTGTGTCTG
TCCACCAGCCACAGCCCAAACACATCAAACCTTGCTAAGCGGCGGATACCCCCAGCTTCTAAG
ATCCCAGCTTCTGCAGTGGAATGCCTGGTTCAGCAGATGTCACAGGATTAAATGTGCAGTT
TGGGGCTCTGGAATTTGGGTGAGAACCTTCTCTCTCTGAATTTGGATCAGCTCCAAGCAGTG
AAAATAGTAATCAGATTCCCATCAGCTTGATTCGAAGTCTTTAAGTGAGCCTTTGAATACA
TCTTTATCAATGACCAGTGCAGTACAGAACTCCACATATACAACCTCCGTCATTACCTCCTG
CAGTCTGACAAGCTCATCACTGAATTCTGCTAGTCCAGTAGCAATGTCTTCCTCTTATGACC
AGAGTTCTGTGCATAACAGGATCCCATACCAAAGCCCTGTGAGTTCATCAGAGTCAGCTCCA
GGAACCATCATGAATGGACATGGTGGTGGTGAAGTCAGCAGACACTAGACAGTAAGTATAG
CAGCAAGCTACTCTTGTCATGGCTGGTGCCAACCAACAGAGGAAGAGGATAGCTCACGTGA
TGTGGAACACACCAGTTGGTCAATGGCTCATTCGTTAAAAAGCAGCCCTTTTGCTTTTTTGT
TTTTGGACCAGGTGTTGGCTGTGGTGTTATTAGAAATGTCTTAACCACAGCAAGAAGGAGGT
GGTGGTCTCATATTCTTCTGCCCTAATCAGACTGCACCACAAGTGCAGCATAACAGTATGCAT
TTTAAAGATGCTTGGGCCAGGCGGGGTGGCTGATGCCATAATCCCAGTGCTTTGGGGGGCC
AAGGCAGGCAGATTGCCCAAGCTCAGGAGTTTGAGACCACCCTGGGCAACATGGTGAACTC
TGTCTCTACTAAAATACGAAAACTAGCCGGGTGTGGTGGCGGCGCGTGCCTGTAATCCCAG
CTACTTGGGAGGCTGAGGCACAAGAATCGCTTGAGCCAGCTTGGGCTACAAAGTGAGACTCC
GTCTGAAAAGA

FIGURE 44

MCFKALGRNSVLLRICSFIPLLKSSVLGSGFGELAPPKMANITSSQILDQLKAPSLGQFTTT
PSTQQNSTSHPTTTTSDWDLKPPTSQSSVLSHLDFKSQPEPSPVLSQLSQRQQHQSQAQVTVPP
PGLESFPSQAKLRESTPGDSPSTVNKLLQLPSTTIENISVSVHQPPKHIKLAKRRIPPASK
IPASAVEMPGSADVTGLNVQFGALEFGSEPSLSEFGSAPSSSENSNQIPISLYSKSLSEPLNT
SLSMTSAVQNSTYTTTSVITSCSLTSSSLNSASPVAMSSSYDQSSVHNRIPTYQSPVSSSESAP
GTIMNGHGGGRSQQTLDISKYSSKLLLSWLVP TKQRKRIAHVMWKTTPVGQWLIR

Signal peptide:

amino acids 1-24

FIGURE 45

GCCGAGTGGGACAAAGCCTGGGGCTGGGCGGGGGCCATGGCGCTGCCATCCCGAATCCTGCT
TTGGAAACTTGTGCTTCTGCAGAGCTCTGCTGTTCTCCTGCACTCAGCGGTGGAGGAGACGG
ACGCGGGGCTGTACACCTGCAACCTGCACCATCACTACTGCCACCTCTACGAGAGCCTGGCC
GTCCGCCTGGAGGTACCGACGGCCCCCGGCCACCCCGCCTACTGGGACGGCGAGAAGGA
GGTGCTGGCGGTGGCGCGCGGGCGACCCGCGCTTCTGACCTGCGTGAACCGCGGGCACGTGT
GGACCGACCGGCACGTGGAGGAGGCTCAACAGGTGGTGCCTGGGACCGGCAGCCGCCCCGGG
GTCCCGCACGACCGCGCGGACCGCCTGCTGGACCTCTACGCGTCGGGCGAGCGCCGCGCCTA
CGGGCCCCCTTTTCTGCGCGACCGCGTGGCTGTGGGCGCGGATGCCTTTGAGCGCGGTGACT
TCTCACTGCGTATCGAGCCGCTGGAGGTGCGCGACGAGGGCACCTACTCCTGCCACCTGCAC
CACCATTACTGTGGCCTGCACGAACGCCGCGTCTTCCACCTGACGGTCGCGGAACCCACGC
GGAGCCGCCCCCGGGGCTCTCCGGGCAACGGCTCCAGCCACAGCGGCGCCCCAGGCCACG
ACCCACACTGGCGCGCGGCCACAACGTCAATGTCATCGTCCCCGAGAGCCGAGCCCAC
TTCTTCCAGCAGCTGGGCTACGTGCTGGCCACGCTGCTGCTCTTCATCCTGCTACTGGTCAC
TGTCTCCTGGCCGCCCCGAGGCGCCGCGGAGGCTACGAATACTCGGACCAGAAGTCGGGAA
AGTCAAAGGGGAAGGATGTTAACTTGGCGGAGTTCGCTGTGGCTGCAGGGGACCAGATGCTT
TACAGGAGTGAGGACATCCAGCTAGATTACAAAAACAACATCCTGAAGGAGAGGGCGGAGCT
GGCCACAGCCCCCTGCCTGCCAAGTACATCGACCTAGACAAAGGGTTCCGGAAGGAGAACT
GCAAATAGGGGAGGCCCTGGGCTCCTGGCTGGGCCAGCAGCTGCACCTCTCCTGTCTGTGCTC
CTCGGGGCATCTCCTGATGCTCCGGGGCTCACCCCTTCCAGCGGTGGTCCCGCTTTCCT
GGAATTTGGCCTGGGCGTATGCAGAGGCCGCTCCACACCCCTCCCCAGGGGCTTGGTGGC
AGCATAGCCCCCACCCTGCGGCCCTTGTCTCACGGGTGGCCCTGCCCACCCCTGGCACAACC
AAAATCCCCTGATGCCCATCATGCCCTCAGACCTTCTGGGCTCTGCCCGCTGGGGGGCCTG
AAGACATTCCTGGAGGACACTCCCATCAGAACCTGGCAGCCCCAAAACCTGGGGTCAGCCTCA
GGGCAGGAGTCCCACTCCTCCAGGGCTCTGCTCGTCCGGGGCTGGGAGATGTTCTTGAGGA
GGACACTCCCATCAGAACTTGGCAGCCTTGAAGTTGGGGTCAGCCTCGGCAGGAGTCCCACT
CCTCCTGGGGTGCTGCCTGCCACCAAGAGCTCCCCACCTGTACCACCATGTGGGACTCCAG
GCACCATCTGTTCTCCCCAGGGACCTGCTGACTTGAATGCCAGCCCTTGCTCCTCTGTGTTG
CTTTGGGGCACCTGGGGCTGCACCCCTGCCCTTTCTCTGCCCCATCCCTACCCTAGCCTTG
CTCTCAGCCACCTTGATAGTCACTGGGCTCCCTGTGACTTCTGACCCTGACACCCCTCCCTT
GGACTCTGCCTGGGCTGGAGTCTAGGGCTGGGGCTACATTTGGCTTCTGTACTGGCTGAGGA
CAGGGGAGGGAGTGAAGTTGGTTTGGGGTGGCCTGTGTTGCCACTCTCAGCACCCACATTT
GCATCTGCTGGTGGACCTGCCACCATCACAATAAAGTCCCCATCTGATTTTTAAAAA
AAAAA

FIGURE 46

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA60618

<subunit 1 of 1, 341 aa, 1 stop

<MW: 38070, pI: 6.88, NX(S/T): 1

MALPSRILLWKLVLQSSAVLLHSAVEETDAGLYTCNLHHHYCHLYESLAVRLEVTDGPPAT
PAYWDGEKEVLAVARGAPALLTCVNRGHVWTD RHVEEAQQVVHWDRQPPGVPHDRADRLDDL
YASGERRAYGPLFLRDRVAVGADAFERGFSLRIEPLVADEGTYSCHLHHHYCGLHERRVF
HLTVAEPHAEPPIRGSPGNGSSHSGAPGPDPTLARGHNVINIVPESRAHFFQQLGYVLATL
LLFILLLVTVLLAARRRRGGYEYSDQKSGKSGKDVNLAEFAVAAGDQMLYRSEDIQLDYKN
NILKERAELAHSPLPAKYIDLDKGFRKENCK

Important features:**Signal peptide:**

amino acids 1-19

Transmembrane domain:

amino acids 237-262

N-glycosylation site.

amino acids 205-208

Cell attachment sequence.

amino acids 151-154

Coproporphyrinogen III oxidase proteins.

amino acids 115-140

46/270

FIGURE 47

CGCCGGAGGCAGCGGCGGCGTGGCGCAGCGGCGACATGGCCGTTGTCTCAGAGGACGACTTT
CAGCACAGTTCAAACCTCACCTACGGAACCACAAGCAGCAGTCTCCGAGCTGACCAGGAGGC
ACTGCTTGAGAAGCTGCTGGACCGCCCGCCCCCTGGCCTGCAGAGGCCCCGAGGACCGCTTCT
GTGGCACATACATCATCTTCTTCAGCCTGGGCATTGGCAGTCTACTGCCATGGAACCTTCTTT
ATCACTGCCAAGGAGTACTGGATGTTCAAACCTCCGCAACTCCTCCAGCCCAGCCACCGGGGA
GGACCTTGAGGGCTCAGACATCCTGAACTACTTTGAGAGCTACCTTGCCGTTGCCTCCACCG
TGCCCTCCATGCTGTGCCTGGTGGCCAACTTCCTGCTTGTCAACAGGGTTGCAGTCCACATC
CGTGTCTTGGCCTCACTGACGGTCATCCTGGCCATCTTCATGGTGATAACTGCACTGGTGAA
GGTGGACACTTCCTCCTGGACCCGTGGTTTTTTTTGCGGTCACCATTGTCTGCATGGTGATCC
TCAGCGGTGCCTCCACTGTCTTCAGCAGCAGCATCTACGGCATGACCGGCTCCTTTCCTATG
AGGAACTCCCAAGCACTGATATCAGGAGGAGCCATGGGCGGGACGGTCAGCGCCGTGGCCTC
ATTGGTGGACTTGCTGCATCCAGTGATGTGAGGAACAGCGCCCTGGCCTTCTTCTTGACGG
CCACCATCTTCCTCGTGCTCTGCATGGGACTCTACCTGCTGCTGTCCAGGCTGGAGTATGCC
AGGTACTACATGAGGCCTGTTCTTGCGGCCCATGTGTTTTCTGGTGAAGAGGAGCTTCCCCA
GGACTCCCTCAGTGCCCTTCGGTGGCCTCCAGATTCATTGATTCCACACACCCCCCTCTCC
GCCCCATCCTGAAGAAGACGGCCAGCCTGGGCTTCTGTGTACCTACGTCTTCTTCATCACC
AGCCTCATCTACCCCGCCGTCTGCACCAACATCGAGTCCCTCAACAAGGGCTCGGGCTCACT
GTGGACCACCAAGTTTTTCATCCCCCTCACTACCTTCCTCCTGTACAACTTTGCTGACCTAT
GTGGCCCGCAGCTCACCGCCTGGATCCAGGTGCCAGGGCCCAACAGCAAGGCGCTCCCAGGG
TTCGTGCTCCTCCGGACCTGCCTCATCCCCCTCTTCGTGCTCTGTAACTACCAGCCCCGCGT
CCACCTGAAGACTGTGGTCTTCCAGTCCGATGTGTACCCCGCACTCCTCAGCTCCCTGCTGG
GGCTCAGCAACGGCTACCTCAGCACCCCTGGCCCTCCTCTACGGGCCTAAGATTGTGCCCAGG
GAGCTGGCTGAGGCCACGGGAGTGGTGATGTCCTTTTATGTGTGCTTGGGCTTAACACTGGG
CTCAGCCTGCTCTACCTCCTGGTGCACCTCATCTAGAAAGGGAGGACACAAGGACATTGGTG
CTTCAGAGCCTTTGAAGATGAGAAGAGAGTGCAGGAGGGCTGGGGGCCATGGAGGAAAGGCC
TAAAGTTTCACTTGGGGACAGAGAGCAGAGCACACTCGGGCCTCATCCCTCCCAAGATGCCA
GTGAGCCACGTCCATGCCCATTCCTGCAAGGCAGATATTCCAGTCATATTAACAGAACT
CCTGAGACAGTTGAAGAAGAAATAGCACAAATCAGGGGTAATCCCTTCACAGCTGATGGTTA
ACATTCCACCTTCTTTCTAGCCCTTCAAAGATGCTGCCAGTGTTTCGCCCTAGAGTTATTACA
AAGCCAGTGCCAAAACCCAGCCATGGGCTCTTTGCAACCTCCCAGCTGCGCTCATTCAGCT
GACAGCGAGATGCAAGCAAATGCTCAGCTCTCCTTACCCTGAAGGGGTCTCCCTGGAATGGA
AGTCCCCTGGCATGGTCAGTCCTCAGGCCCAAGACTCAAGTGTGCACAGACCCCTGTGTTCT
GCGGGTGAACAACTGCCACTAACCAGACTGGAAAACCCAGAAAGATGGGCCTTCCATGAAT
GCTTCATTCCAGAGGGACCAGAGGGCCTCCCTGTGCAAGGGATCAAGCATGTCTGGCCTGGG
TTTTCAAAAAAAGAGGGATCCTCATGACCTGGTGGTCTATGGCCTGGGTCAAGATGAGGGTC
TTTCAGTGTTCTGTTTACAACATGTCAAAGCCATTGGTTCAAGGGCGTAATAAATACTTGC
GTATTCAAAAA

471270

FIGURE 48

MAVVSEDDFQHSSNSTYGTSSSLRADQEALLEKLLDRPPPGQLQRPEDRFCGTYYIIFFSLGI
GSLLPWNFFITAKEYWMFKLRNSSSPATGEDPEGSDILNYFESYLAVASTVPSMLCLVANFL
LVNRVAVHIRVLASLTVILAI FMVITALVKVDTSSWTRGFFAVTIVCMVILSGASTVFSSSI
YGMTGSFPMRNSQALISGGAMGGTVSAVASLVDLAASSDVRNSALAFFLTATIFLVLCMGLY
LLLSRLEYARYYMRPVLAHVFSGEEELPQDSLSAPSVASRFIDSHTPPLRPILKKTASLGF
CVTYVFFITS LIYPAVCTNIESLNKSGSLWTTKFFIPLTTFLLYNFADLCGRQLTAWIQVP
GPNSKALPGFVLLRTCLIPLFVLCNYQPRVHLKTVVFQSDVYPALLSSLLGLSNGYLSTLAL
LYGPKIVPRELAEATGVVMSFYVCLGLTLGSACSTLLVHLI

Transmembrane domain:

amino acids 50-74 (type II), 105-127, 135-153, 163-183, 228-252,
305-330, 448-472

FIGURE 49

GACAGTGGAGGGCAGTGGAGAGGACCGCGCTGTCCTGCTGTCACCAAGAGCTGGAGACACCA
TCTCCCACCGAGAGTCAATGGCCCCATTGGCCCTGCACCTCCTCGTCCTCGTCCCCATCCTCC
TCAGCCTGGTGGCCTCCCAGGACTGGAAGGCTGAACGCAGCCAAGACCCCTTCGAGAAATGC
ATGCAGGATCCTGACTATGAGCAGCTGCTCAAGGTGGTGACCTGGGGGCTCAATCGGACCCT
GAAGCCCCAGAGGGTGATTGTGGTTGGCGCTGGTGTGGCCGGGCTGGTGGCCGCCAAGGTGC
TCAGCGATGCTGGACACAAGGTACCATCCTGGAGGCAGATAACAGGATCGGGGGCCGCATC
TTCACCTACCGGGACCAGAACACGGGCTGGATTGGGGAGCTGGGAGCCATGCGCATGCCAG
CTCTCACAGGATCCTCCACAAGCTCTGCCAGGGCCTGGGGCTCAACCTGACCAAGTTCACCC
AGTACGACAAGAACACGTGGACGGAGGTGCACGAAGTGAAGCTGCGCAACTATGTGGTGGAG
AAGGTGCCCCGAGAAGCTGGGCTACGCCTTGCGTCCCCAGGAAAAGGGCCACTCGCCCCGAAGA
CATCTACCAGATGGCTCTCAACCAGGCCCTCAAAGACCTCAAGGCACTGGGCTGCAGAAAGG
CGATGAAGAAGTTTGAAAGGCACACGCTCTTGGAATATCTTCTCGGGGAGGGGAACCTGAGC
CGGCCGGCCGTGCAGCTTCTGGGAGACGTGATGTCCGAGGATGGCTTCTTCTATCTCAGCTT
CGCCGAGGCCCTCCGGGCCCACAGCTGCCTCAGCGACAGACTCCAGTACAGCCGCATCGTGG
GTGGCTGGGACCTGCTGCCGCGCGCTGCTGAGCTCGCTGTCCGGGCTTGTGCTGTTGAAC
GCGCCCGTGGTGGCGATGACCCAGGGACCGCACGATGTGCACGTGCAGATCGAGACCTCTCC
CCCGGCGCGGAATCTGAAGGTGCTGAAGGCCGACGTGGTGCTGCTGACGGCGAGCGGACCGG
CGGTGAAGCGCATCACCTTCTCGCCGCGCTGCCCCGCCACATGCAGGAGGCGCTGCGGAGG
CTGCACTACGTGCCGGCCACCAAGGTGTTCTTAAGCTTCCGCAGGCCCTTCTGGCGCGAGGA
GCACATTGAAGGCGGCCACTCAAACACCGATCGCCCGTCGCGCATGATTTTCTACCCGCCGC
CGCGCGAGGGCGCGCTGCTGCTGGCCTCGTACACGTGGTCCGACGCGGCGGCAGCGTTCGCC
GGCTTGAGCCGGGAAGAGGCGTTGCGCTTGGCGCTCGACGACGTGGCGGCATTGCACGGGCC
TGTCGTGCGCCAGCTCTGGGACGGCACC GGCGTTCGTCAAGCGTTGGGCGGAGGACCAGCACA
GCCAGGGTGGCTTTGTGGTACAGCCGCGGCGCTCTGGCAAACCGAAAAGGATGACTGGACG
GTCCCTTATGGCCGCATCTACTTTGCCGGCGAGCACACCGCCTACCCGCACGGCTGGGTGGA
GACGGCGGTCAAGTGGCGCTGCGCGCCGCCATCAAGATCAACAGCCGGAAGGGGCCTGCAT
CGGACACGGCCAGCCCCGAGGGGCACGCATCTGACATGGAGGGGCAGGGGCATGTGCATGGG
GTGGCCAGCAGCCCCCTCGCATGACCTGGCAAAGGAAGAAGGCAGCCACCCTCCAGTCCAAGG
CCAGTTATCTCTCCAAAACACGACCCACACGAGGACCTCGCATTAAAGTATTTTCGGAAAAA
AAA

FIGURE 50

MAPLALHLLVLPILLSLVSQDWKAERSQDPFEKCMQDPDYEQLLKVVWGLNRTLKPQRV
IVVGAGVAGLVAAKVLSDAGHKVTILEADNRIGGRIFTYRDQNTGWIGELGAMRMPSSHRIL
HKLCQGLGLNLTKFTQYDKNTWTEVHEVKLRNYVVEKVPEKLGALRPQEKGHSPEDIYQMA
LNQALKDLKALGCRKAMKKFERHTLLEYLLGEGNLSRPAVQLLGDVMSDGGFFYLSFAEALR
AHSCLSDRLOYSRIVGGWDLPLRALLSSLSGLVLLNAPVVAMTQGPHDVHVQIETSPPARNL
KVLKADVLLTASGPAVKRITFSPPLPRHMQEALRRLHYVPATKVFLSFRRPFWRREEHIEGG
HSNTDRPSRMIFYPPPREGALLLASYTWSDAAAAFAGLSREEALRLALDDVAALHGPVVRQL
WDGTGVVKRWAEDQHSQGGFVVQPPALWQTEKDDWTVPYGRIYFAGEHTAYPHGWVETAVKS
ALRAAIKINSRKGPASDTASPEGHASDMEGQGHVHGVASSPSHDLAKEEGSHPPVQGQLSLQ
NTTHTRTSH

Signal peptide:

amino acids 1-21

50/270

FIGURE 51

CTGACATGGCCTGACTCGGGACAGCTCAGAGCAGGGCAGAACTGGGGACACTCTGGGCCGGCCTTCTG
CCTGCATGGACGCTCTGAAGCCACCCTGTCTCTGGAGGAACCACGAGCGAGGGAAGAAGGACAGGGAC
TCGTGTGGCAGGAAGAACTCAGAGCCGGGAAGCCCCATTCACTAGAAGCACTGAGAGATGCGGCCCC
CTCGCAGGGTCTGAATTTCTGCTGCTGTTCAAAAGATGCTTTTTATCTTTAACTTTTTGTTTTCCC
CACTTCCGACCCCGGCGTTGATCTGCATCCTGACATTTGGAGCTGCCATCTTCTTGCGCTGATCACC
AGACCTCAACCCGTCTTACCTCTTCTGACCTGAACAATCAGTCTGTGGGAATTGAGGGAGGAGCAG
GAAGGGGGTTTTCCAGAAGAACAATGACCTAACAAGTTGCTGCTTCTCAGATGCCAAGACTATGTATG
AGGTTTTCCAAAGAGGACTCGCTGTGCTGACAATGGGCCCTGCTTGGGATATAGAAAACCAAACCAG
CCCTACAGATGGCTATCTTACAAACAGGTGTCTGATAGAGCAGAGTACCTGGGTTCCTGTCTCTTGCA
TAAAGTTATAAATCATCACCAGACCAGTTTGTGCGCATCTTTGCTCAGAATAGGCCAGAGTGGATCA
TCTCCGAATTGGCTTGTTACACGTACTCTATGGTAGCTGTACCTCTGTATGACACCTTGGGACCAGAA
GCCATCGTACATATTGTCAACAAGGCTGATATCGCCATGGTGATCTGTGACACACCCCAAAAGGCATT
GGTGCTGATAGGGAATGTAGAGAAAGGCTTCACCCCGAGCCTGAAGGTGATCATCCTTATGGACCCCT
TTGATGATGACCTGAAGCAAAGAGGGGAGAAGAGTGAATGAGATCTTATCCCTATATGATGCTGAG
AACCTAGGCAAAGAGCACTTCAGAAAACCTGTGCCTCCTAGCCCAGAAGACCTGAGCGTCATCTGCTT
CACCAGTGGGACCACAGGTGACCCCAAAGGAGCCATGATAACCCATCAAAATATTGTTTCAAATGCTG
CTGCCTTTCTCAAATGTGTGGAGCATGCTTATGAGCCCACTCCTGATGATGTGGCCATATCCTACCTC
CCTCTGGCTCATATGTTTGAGAGGATTGTACAGGCTGTTGTGTACAGCTGTGGAGCCAGAGTTGGATT
CTTCCAAGGGGATATTGCGTTGCTGGCTGACGACATGAAGACTTTGAAGCCACATTGTTTCCCGCGG
TGCCTCGACTCCTTAACAGGATCTACGATAAGGTACAAAATGAGGCCAAGACACCCCTGAAGAAGTTC
TTGTTGAAGCTGGCTGTTTCCAGTAAATTCAAAGAGCTTCAAAGGGTATCATCAGGCATGATAGTTT
CTGGGACAAGCTCATCTTTGCAAAGATCCAGGACAGCCTGGGCGGAAGGGTTCGTGTAATTGTCACTG
GAGCTGCCCCCATGTCCACTTCAGTCATGACATTCTTCCGGGCAGCAATGGGATGTCAAGTGATGAA
GCTTATGGTCAAACAGAATGCACAGGTGGCTGTACATTTACATTACCTGGGGACTGGACATCAGGTCA
CGTTGGGGTGCCCCCTGGCTTGCAATTACGTGAAGCTGGAAGATGTGGCTGACATGAACACTTTACAG
TGAATAATGAAGGAGAGGTCTGCATCAAGGTACAAACGTGTTCAAAGGATACCTGAAGGACCCTGAG
AAGACACAGGAAGCCCTGGACAGTGATGGCTGGCTTACACAGGAGACATTGGTTCGCTGGCTCCCGAA
TGGAACCTCTGAAGATCATCGACCGTAAAAAGAACATTTTCAAGCTGGCCCAAGGAGAATACATTGCAC
CAGAGAAGATAGAAAATATCTACAACAGGAGTCAACCAGTGTTACAAATTTTTGTACACGGGGAGAGC
TTACGGTCATCCTTAGTAGGAGTGGTGGTTTCTGACACAGATGTACTTCCCTCATTTGCAGCCAAGCT
TGGGGTGAAGGGCTCCTTTGAGGAACTGTGCCAAAACCAAGTTGTAAGGGAAGCCATTTTAGAAGACT
TGCAGAAAATTGGGAAGAAAGTGGCCTTAAACTTTTGAACAGGTCAAAGCCATTTTCTTCATCCA
GAGCCATTTTCCATTGAAAATGGGCTCTTGACACCAACATTGAAAGCAAAGCGAGGAGAGCTTCCAA
ATACTTTCGGACCCAAATTGACAGCCTGTATGAGCACATCCAGGATTAGGATAAGGTACTTAAGTACC
TGCCGGCCCACTGTGCACTGCTTGTGAGAAAATGGATTAAAACTATTCTTACATTTGTTTTGCCTTT
CCTCCTATTTTTTTTTTAACCTGTTAAACTCTAAAGCCATAGCTTTTGTTTTATATTGAGACATATAAT
GTGTAAACTTAGTTCCCAAATAAATCAATCCTGTCTTTCCCATCTTCGATGTTGCTAATATTAAGGCT
TCAGGGCTACTTTTATCAACATGCCTGTCTTCAAGATCCCAGTTTATGTTCTGTGCTTCTCCTCATGA
TTTCCAACCTTAATACTATTAGTAACCACAAGTTCAAGGGTCAAAGGGACCCCTCTGTGCCTTCTTCTT
TGTTTTGTGATAAACATAAATTGCCAACAGTCTCTATGCTTATTTACATCTTCTACTGTTCAAACATAA
GAGATTTTTAAATTCTGAAAACTGCTTACAATTATGTTTTCTAGCCACTCCACAAACCACTAAAT
TTTAGTTTTAGCCTATCACTCATGTCAATCATATCTATGAGACAAATGTCTCCGATGCTCTTCTGCGT
AAATTAAATTGTGTACTGAAGGGAAAAGTTTGATCATACCAAACATTTCTAAACTCTCTAGTTAGAT
ATCTGACTTGGGAGTATTAATAAATTGGGTCTATGACATACTGTCCAAAAGGAATGCTGTTCTTAAAGC
ATTATTTACAGTAGGAACTGGGGAGTAAATCTGTTCCCTACAGTTTGCTGCTGAGCTGGAAGCTGTGG
GGGAAGGAGTTGACAGGTGGGCCCAGTGAACTTTTCCAGTAAATGAAGCAAGCACTGAATAAAAACCT
CCTGAACCTGGGAACAAAGATCTACAGGCAAGCAAGATGCCACACAACAGGCTTATTTTCTGTGAAGG
AACCAACTGATCTCCCCACCCTTGGATTAGAGTTCCTGCTCTACCTTACCCACAGATAACACATGTT
GTTTCTACTTGTAATGTAAAGTCTTTAAATAAATATTACAGATAAAAAA

FIGURE 52

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA60775
<subunit 1 of 1, 739 aa, 1 stop
<MW: 82263, pI: 7.55, NX(S/T): 3
MDALKPPCLWRNHERGKKDRDSCGRKNSEPGSPHSLEALRDAAPSQGLNLLLLFTKMLFIFN
FLFSPLPTPALICILTFGAAIFLWLITRPQPVLPDLLNNSVGIEGGARKGVSQKNNDLTS
CCFSDAKTMYEVFQRGGLAVSDNGPCLGYRKPNQPYRWLSYKQVSDRAEYLGSCLLHKGYKSS
PDQFVGIFAQNRPEWIISELACYTYSMVAVPLYDTLGPEAIVHIVNKADIAMVICDTPQKAL
VLIGNVEKGFTPSLKVIIIMDPFDDDLKQRGEKSGIEILSLYDAENLGKEHFRKPVPPSPED
LSVICFTSGTTGDPKGAMITHQNIVSNAAFLKCVEHAYEPTPDDVAISYLPLAHMFERIVQ
AVVYSCGARVGFFQGDIRLLADDMLKPTLFPVPRLLNRIYDKVQNEAKTPLKKFLLKLA
VSSKFELQKGIIRHDSFWDKLI FAKIQDSLGRVRVIVTGAAPMSTSVMTFFRAAMGCQVY
EAYGQTECTGGCTFTLPGDWTSGHVGVPACNYVKLEDVADMNYFTVNNEGEVCIKGTNVFK
GYLKDPEKTQEALDSGWLHTGDIGRWLPNGTLKIIDRKKNIFKLAQGEYIAPEKIENIYNR
SQPVLQIFVHGESLRSSLVGVVVPDPTDVLPSFAAKLGVKGSFEELCQNQVVREAILEDLQKI
GKESGLKTFEQVKAIFLHPEPFSEIENGLLTPTLKAARGELSKYFRTQIDSLYEHIQD

Important features:**Type II transmembrane domain:**

amino acids 61-80

Putative AMP-binding domain signature.

amino acids 314-325

N-glycosylation site.

amino acids 102-105, 588-591 and 619-622

52/270

FIGURE 53

GGAGGCGGAGGCCGCGGCGAGCCGGGCGGAGCAGTGAGGGCCCTAGCGGGGCCCCGAGCGGGG
CCCCGGGGCCCCCTAAGCCATTCCCTGAAGTCATGGGCTGGCCAGGACATTGGTGACCCGCCAAT
CCGGTATGGACGACTGGAAGCCCAGCCCCCTCATCAAGCCCTTTGGGGCTCGGAAGAAGCGG
AGCTGGTACCTTACCTGGAAGTATAAACTGACAAACCAGCGGGCCCTGCGGAGATTCTGTCA
GACAGGGGCCCGTGCTTTTCTGTGCTGGTGACTGTCATTGTCAATATCAAGTTGATCCTGGACA
CTCGGCGAGCCATCAGTGAAGCCAATGAAGACCCAGAGCCAGAGCAAGACTATGATGAGGCC
CTAGGCCGCTGGAGCCCCACGGCGCAGAGGCAGTGGTCCCCGGCGGGTCTTGGACGTAGA
GGTGTATTCAAGTCGCAGCAAAGTATATGTGGCAGTGGATGGCACCACGGTGCTGGAGGATG
AGGCCCGGGAGCAGGGCCGGGGCATCCATGTATTGTCTCAACCAGGCCACGGGCCACGTG
ATGGCAAACGTGTGTTTGACACGTACTCACCTCATGAGGATGAGGCCATGGTGCTATTCTCT
CAACATGGTAGCGCCCGGCCGAGTGCTCATCTGCACTGTCAAGGATGAGGGCTCCTTCCACC
TCAAGGACACAGCCAAGGCTCTGCTGAGGAGCCTGGGCAGCCAGGCTGGCCCTGCCCTGGGC
TGGAGGGACACATGGGCCTTCGTGGGACGAAAAGGAGGTCTGTCTTCGGGGAGAAACATTC
TAAGTCACCTGCCCTCTCTTCTGGGGGGACCCAGTCTGTCTGAAGACAGATGTGCCATTGA
GCTCAGCAGAAGAGGCAGAGTGCCACTGGGCAGACACAGAGCTGAACCGTCGCCGCCGGCGC
TTCTGCAGCAAAGTTGAGGGCTATGGAAGTGTATGCAGCTGCAAGGACCCACACCCATCGA
GTTTACGCCCTGACCCACTCCCAGACAACAAGTCTCAATGTGCCTGTGGCTGTCAATTGCAG
GGAACCGACCCAATTACCTGTACAGGATGCTGCGCTCTCTGCTTTCAGCCCAGGGGGTGTCT
CCTCAGATGATAACAGTTTTTCATTGACGGCTACTATGAGGAACCCATGGATGTGGTGGCACT
GTTTGGTCTGAGGGGCATCCAGCATACTCCCATCAGCATCAAGAATGCCCGCGTGTCTCAGC
ACTACAAGGCCAGCCTCACTGCCACTTTCAACCTGTTTCCGGAGGCCAAGTTTGTCTGTGGT
CTGGAAGAGGACCTGGACATTGCTGTGGATTTTTTTCAGTTTCTGAGCCAATCCATCCACCT
ACTGGAGGAGGATGACAGCCTGTACTGCATCTCTGCCTGGAATGACCAGGGGTATGAACACA
CGGCTGAGGACCCAGCACTACTGTACCGTGTGGAGACCATGCCTGGGCTGGGCTGGGTGCTC
AGGAGGTCCTTGTACAAGGAGGAGCTTGAGCCCAAGTGGCCTACACCGGAAAAGCTCTGGGA
TTGGGACATGTGGATGCGGATGCCTGAACAACGCCGGGGCCGAGAGTGATCATCCCTGACG
TTTCCCGATCCTACCACCTTTGGCATCGTCGGCCTCAACATGAATGGCTACTTTACAGAGGCC
TACTTCAAGAAGCACAAAGTTCAACACGGTTCCAGGTGTCCAGCTCAGGAATGTGGACAGTCT
GAAGAAAGAAGCTTATGAAGTGGAAGTTCACAGGCTGCTCAGTGAGGCTGAGGTTCTGGACC
ACAGCAAGAACCTTGTGAAGACTCTTTCTGCCAGACACAGAGGGCCACACCTACGTGGCC
TTTATTTCGAATGGAGAAAGATGATGACTTCACCACCTGGACCCAGCTTGCCAAGTGCCTCCA
TATCTGGGACCTGGATGTGCGTGGCAACCATCGGGCCTGTGGAGATTGTTTCGGAAGAAGA
ACCACTTCTGGTGGTGGGGTCCCGGCTTCCCCCTACTCAGTGAAGAAGCCACCCTCAGTC
ACCCCAATTTTCTGGAGCCACCCCCAAAGGAGGAGGGAGCCCCAGGAGCCCCAGAACAGAC
ATGAGACCTCCTCCAGGACCCCTGCGGGGCTGGGTACTGTGTACCCCCAGGCTGGCTAGCCCT
TCCCTCCATCCTGTAGGATTTTGTAGATGCTGGTAGGGGCTGGGGCTACCTTGTTTTAAACA
TGAGACTTAATTACTAACTCCAAGGGGAGGGTTCCCCTGCTCCAACACCCCGTTCCTGAGTT
AAAAGTCTATTTATTTACTTCTTGTGGAGAAGGGCAGGAGAGTACCTGGGAATCATTACG
ATCCCTAGCAGCTCATCCTGCCCTTTGAATAACCTCACTTTCCAGGCCTGGCTCAGAATCTA
ACCTATTTATTGACTGTCTGAGGGCCTTGAAAACAGGCCGAACCTGGAGGGCCTGGATTTT
TTTTTGGGCTGGAATGCTGCCCTGAGGGTGGGGCTGGCTCTTACTCAGGAACTGCTGTGCC
CAACCCATGGACAGGCCCAGCTGGGGCCCATGCTGACACAGACTCACTCAGAGACCCTTA
GACACTGGACCAGGCCTCCTCTCAGCCTTCTCTTTGTCCAGATTTCCAAAGCTGGATAAGTT
GGTCATTGATTAAAAAAGGAGAAGCCCTCTGGGAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 54

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA61185
><subunit 1 of 1, 660 aa, 1 stop
><MW: 75220, pI: 6.76, NX(S/T): 0
MDDWKPSPLIKPFGARKKRSWYLTWKYKLTNQALRRFCQTGAVLFLLVTVIVNIKLILDTR
RAISEANEDPEPEQDYDEALGRLEPPRRRGSGPRRVLDVEVYSSRSKVYVAVDGTTVLEDEA
REQGRGIHVIVLNQATGHVMAKRVFDTYSPHEDEAMVLFLNMVAPGRVLICTVKDEGSFHLK
DTAKALLRSLGSQAGPALGWRDTWAFVGRKGGPVFGKHSKSPALSSWGDPLVLLKTDVPLSS
AEEAECHWADTELNRRRRRRFC SKVEGYGSVCCKDPTPIEFSPDPLPDNKVLNVPVAVIAGN
RPNYLYRMLRSLLSAQGVSPQMITVFI DGYEPM DVVALFGLRGIQHTPISIKNARVSQHY
KASLTATFNLFPEAKFAVVLEEDLDIAVDFFSFLSQSIHLLEEDDSLYCISAWNDQGYEHTA
EDPALLYRVETMPGLGWVLRRLSYKEELEPKWPTPEKLWDWDMWMRMPEQRRGRECIIPDVS
RSYHFGIVGLNMNGYFHEAYFKKHKFNTVPGVQLRNVDLKKKEAYEVEVHRLLEAEVLDHS
KNPCEDSFLPDTEGHTYVAFIRMEKDDDDFTTWTQLAKCLHIWDL DVRGNHRGLWRLFRKKNH
FLVVGVPASPYSVKKPPSVTPIFLEPPPKEEGAPGAPEQT

Important features of the protein:**Transmembrane domain:**

amino acids 38-55

Homologous region to Mouse GNT1

amino acids 229-660

54/270

FIGURE 55

CGGACGCGTGGGCTGCTGGTGGGAAGGCCTAAAGAACTGGAAAGCCCACTCTCTTGGAAACCACCACAC
CTGTTTAAAGAACCTAAGCACCATTAAAGCCACTGGAAATTTGTTGTCTAGTGGTTGTGGGTGAATA
AAGGAGGGCAGAAATGGATGATTTTCATCTCCATTAGCCTGCTGTCTCTGGCTATGTTGGTGGGATGTTA
CGTGGCCGGAATCATTCCTTTGGCTGTTAATTTCTCAGAGGAACGACTGAAGCTGGTGACTGTTTTGG
GTGCTGGCCTTCTCTGTGAACTGCTCTGGCAGTCATCGTGCCTGAAGGAGTACATGCCCTTTATGAA
GATATTTCTTGAGGGAAAACACCACCAAGCAAGTGAAACACATAATGTGATTGCATCAGACAAAGCAGC
AGAAAAATCAGTTGTCCATGAACATGAGCAGCCACGACCACACACAGCTGCATGCCTATATTGGTG
TTTCCCTCGTTCTGGGCTTCGTTTTCATGTTGTCTGGTGGACCAGATTGGTAACTCCCATGTGCATTCT
ACTGACGATCCAGAAGCAGCAAGGTCTAGCAATTCCAAAAATCACCACCACGCTGGGTCTGGTTGTCCA
TGCTGCAGCTGATGGTGTGCTTTGGGAGCAGCAGCATCTACTTCACAGACCAGTGTCCAGTTAATTG
TGTTTGTGGCAATCATGCTACATAAGGCACCAGCTGCTTTTGGACTGGTTTCCTTCTTGATGCATGCT
GGCTTAGAGCGGAATCGAATCAGAAAGCACTTGCTGGTCTTTGCATTGGCAGCACCAGTTATGTCCAT
GGTGACATACTTAGGACTGAGTAAGAGCAGTAAAGAAGCCCTTTAGAGGTGAACGCCACGGGAGTGG
CCATGCTTTTCTGCGGGGACATTTCTTTATGTTGCCACAGTACATGTCCTCCCTGAGGTGGGCGGA
ATAGGGCACAGCCACAAGCCGATGCCACGGGAGGGAGAGGCCTCAGCCGCTGGAAGTGGCAGCCCT
GGTTCTGGGTTGCCCTCATCCCTCTCATCCTGTGCTAGGACACCAGCATTAATGTTCAAGGTCCAGC
CTTGGTCCAGGGCCGTTTGCCATCCAGTGAGAACAGCCGGCACGTGACAGCTACTCACTTCTCAGTC
TCTTGTCTCACCTTGCGCATCTCTACATGTATTCTAGAGTCCAGAGGGGAGGTGAGGTAAACCTG
AGTAATGGAAAAGCTTTTAGAGTAGAAAACATTTACGTTGCAGTTAGCTATAGACATCCATTGTGT
TATCTTTTAAAGGCCCTTGACATTTTGCGTTTTAATATTTCTCTTAACCCTATTCTCAGGGAAGATG
GAATTTAGTTTTAAGGAAAAGAGGAGAACTTCATACTCACAATGAAATAGTGATTATGAAAATACAGT
GTTCTGTAATTAAGCTATGTCTCTTCTTCTTAGTTTAGAGGCTCTGCTACTTTATCCATTGATTTTT
AACATGGTTCCACCATGTAAGACTGGTGCTTTAGCATCTATGCCACATGCGTTGATGGAAGGTATA
GCACCCACTCACTTAGATGCTAAAGGTGATTCTAGTTAATCTGGGATTAGGGTCAGGAAAATGATAGC
AAGACACATTGAAAGCTCTCTTTATACTCAAAGAGATATCCATTGAAAAGGGATGCTAGAGGGATT
TAAACAGCTCCTTTGGCACGTGCCTCTCTGAATCCAGCCTGCCATTCCATCAAATGGAGCAGGAGAGG
TGGGAGGAGCTTCTAAAGAGGTGACTGGTATTTTGTAGCATTCTTGTCAAGTTCTCCTTTGCAGAAT
ACCTGTCTCCACATTCCTAGAGAGGAGCCAAGTTCTAGTAGTTTCAGTTCTAGGCTTTCCCTTCAAGAA
CAGTCAGATCACAAAGTGTCTTTGGAAATTAAGGGATATTAATTTTAAAGTGATTTTGGATGGTTAT
TGATATCTTTGTAGTAGCTTTTTTTTAAAGACTACCAAATGTATGGTTGTCCTTTTTTTTTTGT
TTTTTTTTTAATTATTTCTCTTAGCAGATCAGCAATCCCTCTAGGGACCTAAATACTAGGTGAGCTTT
GGCGACACTGTGTCTTCTCACATAACCACCTGTAGCAAGATGGATCATAAATGAGAAGTGTGCTTA
TTGATTTAAAGCTTATTGGAATCATGTCTCTTGTCTCTTCGTCTTTTCTTTGCTTTTCTTCTAACTTT
TCCCTCTAGCCTCTCCTCGCCACAATTTGCTGCTTACTGCTGGTGTAAATATTTGTGTGGGATGAATT
CTTATCAGGACAACCCTTCTCGAAGTGAATAATGAAGATAATAATATCTTTATCTTTATCCCTT
CAAAGAAATTACCTTTGTGTCAAATGCCGCTTTGTTGAGCCCTTAAATACCACCTCCTCATGTGTAA
ATTGACACAATCACTAATCTGGTAATTTAAACAATTGAGATAGCAAAAGTGTTTAACAGACTAGGATA
ATTTTTTTTTCATATTTGCCAAAATTTTGTAAACCCTGTCTTGTCAAATAAGTGTATAATATTGTAT
TATTAATTTATTTTACTTTCTATACCATTTCAAACACATTACCTAAGGGGGAACCAAGACTAGTT
TCTTCAGGGCAGTGGACGTAGTAGTTTGTAAAAACGTTTTCTATGACGCATAAGCTAGCATGCCTATG
ATTTATTTCTTTTATGAATTTGTCACTGGATCAGCAGCTGTGGAAATAAAGCTTGTGAGCCCTGTGCT
GGCCACAGTGAAGGAAAGTAGCACAATAAGGATACAGTTGTATGTAGTCATTGGCAACAAATGTCATACA
ATTTTACTACCAAGAGAAGGTATAGTATGGAAAGTCCAAATGACTTCCTTGATTGGATGTTAACAGCT
GACTGGTGTGAGACTTGAGTTTTCTAGTCCTTCAAACCTATATGGTTGCCTAGATTCTCTCTGGA
AACTGACTTTGTCAAATAAATAGCAGATTGTAGTGTCAAAAAA

FIGURE 56

MDDFISISLLSLAMLVGCYVAGIIPLAVNFSEERLKLVTVLGAGLLCGTALAVIVPEGVHAL
YEDILEGKHHQASETHNVIASDKAAEKSVVHEHEHSHDHTQLHAYIGVSLVLGFVFMLLVDQ
IGNSHVHSTDDPEAARSSNSKITTTTGLVHVHAAADGVALGAAASTSQTSVQLIVFVAIMLHK
APAAFGLVSFLMHAGLERNRIRKLLVFALAAPVMSMVTYLGLSKSSKEALSEVNATGVAML
FSAGTFLYVATVHVLPEVGGIGHSHKPDATGGRGLSRLEVAALVLGCLIPILISVGHQH

Signal peptide:

amino acids 1-18

Transmembrane domain:

amino acids 37-56, 106-122, 211-230, 240-260, 288-304

FIGURE 57

GCTCGAGGCCGCGGCGGCGGGAGAGCGACCCGGGCGGCCTCGTAGCGGGGCCCCGGATCCC
CGAGTGGCGGCCGGAGCCTCGAAAAGAGATTCTCAGCGCTGATTTTGAGATGATGGGCTTGG
GAAACGGGCGTCGCAGCATGAAGTCGCCGCCCTCGTGCTGGCCGCCCTGGTGGCCTGCATC
ATCGTCTTGGGCTTCAACTACTGGATTGCGAGCTCCCGGAGCGTGACCTCCAGACACGGAT
CATGGAGCTGGAAGGCAGGGTCCGCAGGGCGGCTGCAGAGAGAGGCGCCGTGGAGCTGAAGA
AGAACGAGTTCCAGGGAGAGCTGGAGAAGCAGCGGGAGCAGCTTGACAAAATCCAGTCCAGC
CACAACCTTCCAGCTGGAGAGCGTCAACAAGCTGTACCAGGACGAAAAGGCGGTTTTTGGTGAA
TAACATCACCACAGGTGAGAGGCTCATCCGAGTGCTGCAAGACCAGTTAAAGACCCTGCAGA
GGAATTACGGCAGGCTGCAGCAGGATGTCCTCCAGTTTTCAGAAGAACCAGACCAACCTGGAG
AGGAAGTTCTCCTACGACCTGAGCCAGTGCATCAATCAGATGAAGGAGGTGAAGGAACAGTG
TGAGGAGCGAATAGAAGAGGTCACCAAAAAGGGGAATGAAGCTGTAGCTTCCAGAGACCTGA
GTGAAAACAACGACCAGAGACAGCAGCTCCAAGCCCTCAGTGAGCCTCAGCCCAGGCTGCAG
GCAGCAGGCCTGCCACACACAGAGGTGCCACAAGGGAAGGGAACGTGCTTGTTAACAGCAA
GTCCCAGACACCAGCCCCCAGTTCCGAAGTGGTTTTTGATTCAAAGAGACAAGTTGAGAAAG
AGGAAACCAATGAGATCCAGGTGGTGAATGAGGAGCCTCAGAGGGACAGGCTGCCGCAGGAG
CCAGGCCGGGAGCAGGTGGTGGGAAGACAGACCTGTAGGTGGAAGAGGCTTCGGGGGAGCCGG
AGAACTGGGCCAGACCCACAGGTGCAGGCTGCCCTGTCAGTGAGCCAGGAAAATCCAGAGA
TGGAGGGCCCTGAGCGAGACCAGCTTGTATCCCCGACGGACAGGAGGAGGAGCAGGAAGCT
GCCGGGGAAGGGAGAAACCAGCAGAACTGAGAGGAGAAGATGACTACAACATGGATGAAAA
TGAAGCAGAATCTGAGACAGACAAGCAAGCAGCCCTGGCAGGGAATGACAGAAACATAGATG
TTTTTAATGTTGAAGATCAGAAAAGAGACACCATAAATTTACTTGATCAGCGTGAAAAGCGG
AATCATACACTCTGAATTGAACTGGAATCACATATTTACAACAGGGCCGAAGAGATGACTA
TAAAATGTTTCATGAGGGACTGAATACTGAAAACGTGAAATGTACTAAATAAAATGTACATCTGA

FIGURE 58

MMGLGNGRRSMKSPPLVLAALVACIIIVLGFNYWIIASSRSVDLQTRIMELEGRVRRAAAERGA
VELKKNEFQGELEKQREQLDKIQSSHNFQLESVNKLYQDEKAVLVNNITTGERLIRVLQDQL
KTLQRNYGRLQQDVLQFQKNQTNLERKFSYDLSQCINQMKEVKEQCEERIEEVTKKGNEAVA
SRDLSENNDQRQQLQALSEPQPRLQAAGLPHTTEVPQGKGNVLGNSKSQTPAPSSEVVLDSKR
QVEKEETNEIQVVNEEPQRDRLPQEPGREQVVEDRPVGGRGFGGAGELGQTPQVQAALSVSQ
ENPEMEGPERDQLVIPDGQEEEQEAAGEGRNQKLRGEDDYNMDENEAESETDKQAALAGND
RNIDVFNVEDQKRDTINLLDQREKRNHTL

Signal peptide:

amino acids 1-29

FIGURE 59

GGATGCAGAAAGCCTCAGTGTGCTCTTCTGGCCTGGGTCTGCTTCTTCTACGCTGGCATTGCCCTCTTCA
CCAGTGGCTTCTCTGCTCACCCGTTTGGAGCTCACCAACCATAGCAGCTGCCAAGAGCCCCAGGCCCTGGGTCCC
TGCCATGGGGGAGCCAAGGAAACCTGGGGCCTGCTGGATGGCTTCCCATTTCGCGGGTGTGTGGTGTCTGA
TAGATGCTCTGCGATTTGACTTCGCCCAGCCCCAGCATTACACGCTGCCTAGAGAGCCTCTGTCTCCCTACCCT
TCCTGGGCAAACTAAGCTCCTTGACAGAGATCCTGGAGATTACAGCCCCACCATGCCGGCTCTACCGATCTCAGG
TTGACCCCTCTACCACCACCATGCAGCGCCTCAAGGCCCTCACCACTGGCTCACTGCCTACCTTTATTGATGCTG
GTAGTAACTTCGCCAGCCAGCCCATAGTGAAGACAATCTCATTAAGCAGCTCACCACTGCAGGAAGGCGTGTAG
TCTTCATGGGAGATGATACCTGGAAAGACCTTTTCCCTGGTGTCTTCTCCAAAGCTTCTTCTTCCCATCTTCA
ATGTCAGAGACCTAGACACAGTGGACAATGGCATCTTGGAAACACCTCTACCCACCATGGACAGTGGTGAATGGG
ACGTGCTGATTGCTCACTTCTGGGTGTGGACCACCTGTGGCCACAAGCATGGCCCTCACCACTGAAATGGCCA
AGAAACTTAGCCAGATGGACCAGGTGATCCAGGGACTTGTGGAGCGTCTGGAGAATGACACACTGCTGGTAGTGG
CTGGGGACCATGGGATGACCACAAATGGAGACCATGGAGGGGACAGTGAGCTGGAGGTCTCAGCTGCTCTCTTTC
TGTATAGCCCCACAGCAGTCTTCCCCAGCACCCACCAGAGGAGCCAGAGGTGATTCTCAAGTTAGCCTTGTGC
CCACGCTGGCCCTGCTGCTGGGCCTGCCATCCCATTGGGAATATCGGGGAAGTGTGGCTGAGCTATTCTCAG
GGGTGAGGCTCCCGAGCCCCACTCCTCTGCTTTAGCCCAAGCCTCAGCTCTCCATCTCAATGCTCAGCAGGTGT
CCCGATTTCTCATACCTACTCAGCTGCTACTCAGGACCTTCAAGCTAAGGAGCTTCATCAGCTGCAGAACCTCT
TCTCCAAGCCCTCTGCTGACTACCACTGGCTTCTCCAGAGCCCCAAGGGGGCTGAGGCGACACTGCCGACTGTGA
TTGCTGAGCTGCAGCAGTTCTTGGGGGAGCTCGGGCCATGTGCATCGAGTCTTGGGCTCGTTCTCTCTGGTCC
GCATGGCGGGGGTACTGCTCTCTTGGCTGCTTCTGCTTTATCTGCTGCTGGCATCTCAGTGGGCAATATCCC
CAGGCTTTCCATCTCTGCCCTTACTCCTGACACCTGTGGCCTGGGGCCTGGTTGGGGCCATAGCGTATGCTGGAC
TCCTGGGAACATTGAGCTGAAGCTAGATCTAGTGCTTCTAGGGGCTGTGGCTGCAGTGAGCTCATTCTCCCTT
TTCTGTGGAAGCCTGGGCTGGCTGGGGGTCCAAGAGGCCCTGGCAACCCTGTTTCCCATCCCTGGGCCCCGTCC
TGTTACTCTCTGCTGTTTCGCTTGGCTGTGTTCTTCTCTGATAGTTTGTGTGAGCTGAGGCCAGGGCCACCCCT
TCCTTTTGGGCTCATTCTCTGCTCCTGGTGTGTCAGCTTCACTGGGAGGGCCAGCTGCTTCCACCTAAGCTAC
TCAATATGCCCCGCTTGGCACTTCAGCCACAACAACCCCCACGGCACAATGGTGCAATATGCCCTGAGGCTTG
GAATTGGGTGTCTTTATGTACAAGCTAGCTGGGCTTTTTCATCGTTGCCCTGAAGAGACACCTGTTTGCCACT
CCTCTCCCTGGCTGAGTCTCTGGCATCCATGGTGGGTGGTGCAGCCAAGAATTTATGGTATGGAGCTTGTGTGG
CGGCGCTGGTGGCCCTGTTAGCTGCCGTGCGCTTGTGGCTTCGCCCTATGGTAATCTCAAGAGCCCCGAGCCAC
CCATGCTCTTTGTGCGCTGGGGACTGCCCTAATGGCATTGGGTACTGCTGCCTACTGGGCATTGGCGTGGGGG
CAGGCTTCCCTGCTCCTGGGTCTCGGGTCTGCTGCTCTGGGGCATCCATGGTGCTGCCTCGGGCTGAGCAGGGC
TGGCTGCTTCAGGGCTCGCGCTGCTGCTCTGGAAGCCTGTGACAGTGTGGTGAAGGCTGGGGCAGGCGCTCCAA
GGACCAGGACTGTCTCACTCCCTTCTCAGGCCCCCCCCACTTCTCAAGCTGACTTGGATTATGTGGTCCCTCAA
TCTACCGACACATGCAGGAGGAGTTCCGGGGCCGGTTAGAGAGGACCAATCTCAGGGTCCCTGACTGTGGCTG
CTTATCAGTTGGGGAGTGTCTACTCAGCTGCTATGGTCACAGCCCTCACCTGTTGGCCTTCCCACTTCTGCTGT
TGCATGCGGAGCGCATCAGCCTTGTGTTCTGCTTCTGTTTCTGCGAGAGCTTCTTCTCTACATCTGCTTGTG
CTGGGATACCCGTCACCAACCCCTGGTCTTTTACTGTGCCATGGCAGGCAGTCTCGGCTTGGGCCCTCATGGCCA
CACAGACCTTCTACTCCACAGGCCACCAGCCTGTCTTTCAGCCATCCATTGGCATGCAGCCTTCGTGGGATTCC
CAGAGGGTATGGCTCCTGTACTTGGCTGCCTGCTTTGCTAGTGGGAGCCAACACCTTTGCTTCCACCTCTCT
TTGCAGTAGGTGCCCCACTGCTCCTGCTCTGGCCTTCTCTGTGTGAGAGTCAAGGGCTGCGGAAGAGACAGCAGC
CCCCAGGGAATGAAGCTGATGCCAGAGTCAGACCCGAGGAGGAAGAGGAGCCACTGATGGAGATCGGGCTCCGGG
ATGCGCCTCAGCACTTCTATGCAGCACTGCTGCAGCTGGGCCTCAAGTACCTCTTTATCTTGGTATTTCAGATT
TGGCCTGTGCCTTGGCAGCCTCCATCCTTCGAGGCATCTCATGGTCTGGAAAGTGTGTTGCCCTAAGTTTCATAT
TTGAGGCTGTGGGCTTCATTGTGAGCAGCGTGGGACTTCTCCTGGGCATAGCTTTGGTGATGAGAGTGGATGGT
CTGTGAGCTCCTGGTTCAGGCAGCTATTTCTGGCCAGCAGAGGTAGCCTAGTCTGTGATTACTGGCACTTGGCT
ACAGAGAGTCTGGAGAACAGTGTAGCCTGGCCTGACAGGTACTGGATGATCTGCAAGACAGGCTCAGCCATAC
TCTTACTATCATGCAGCCAGGGGCCGCTGACATCTAGGACTTCATTATCTATAATTACAGACCACAGTGGAGTA
TGATCCCTAACTCCTGATTTGGATGCATCTGAGGGACAAGGGGGCGGTCTCCGAAGTGAATAAAATAGGCCGG
GCGTGGTGACTTGACCTATAATCCCAGCACTTTGGGAGGCAGAGGTGGGAGGATTGCTTGGTCCCAGGAGTTCA
AGACCAGCCTGTGGAACATAACAAGACCCCGTCTCTACTATTTAAAAAAAGTGAATAAAATGATAATAT

FIGURE 60

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA62809

<subunit 1 of 1, 1089 aa, 1 stop

<MW: 118699, pI: 8.49, NX(S/T): 2

MQKASVLLFLAWVCFLFYAGIALFTSGFLLTRLELTNHSSCQEPGPGSLPWGSQGKPGACW
MASRFSRVVLVLIDALRFDFAQPQHSHVPREPPVSLPFLGKLSSLQRILEIQPHHARLYRSQ
VDPPTTTMQRLKALTGSLPTFIDAGSNFASHAIVEDNLIKQLTSAGRRVVFMGDDTWKDLF
PGAFSKAFFFPFNFVRDLDTVDNGILEHLYPTMDSGEWDVLIHFLGVHDHCGHKHGHHPHEM
AKKLSQMDQVIQGLVERLENDTLLVVAGDHGMMTNGDHGGDSELEVSAALFLYSPTAVFPST
PPEEPEVLPQVSLVPTLALLLGLPIPFNGI GEVMAELFSGGEDSQPHSSALAQASALHLNAQ
QVSRFLHTYSAATQDLQAKELHQLQNLFSKASADYQWLLQSPKGAEATLPTVIAELQQFLRG
ARAMCIESWARFSLVRMAGGTALLAASCFCILLASQWAI SPGFPPCPLLLTPVAWGLVGAIA
YAGLLGTIELKLDLVLLGAVAAVSSFLPFLWKAWAGWGSKRPLATLFPPIPGPVLLLLLFRLA
VFFSDSFVVAEARATPFLGSGFILLVVQLHWEGQLLPKLLTMPRLGTSATTNPPRHNGAY
ALRLGIGLLLLCTRLAGLFHRCPEETPVCHSSPWLSPLASMVGGRAKNLWYGACVAALVALLA
AVRLWLRRYGNLKSPEPPMLFVRWGLPLMALGTAAYWALASGADEAPPRLRVLVSGASMVLP
RAVAGLAASGLALLLWKPVTVLVKAGAGAPRTRTVLTPFSGPPTSQADLDYVVPQIYRHMQE
EFRGRLETKSQGPLTVAAYQLGSVYSAAMVTALTLLAFPLLLLHAERISLVFLLLFLQSFL
LLHLLAAGIPVTTTPGPFTVPWQAVSAWALMATQTFYSTGHQPVFPAIHWHA AFVGFPEGHGS
CTWLPALLVGANTFASHLLFAVGCPLLLLPFLCESQGLRKRQPPGNEADARVRPEEEEEEP
LMEMRLRDAPQHFYAALLQLGLKYLFI LGI QILACALAASILRRHLMVWKVFAPKFI FEAVG
FIVSSVGLLLGIALVMRVDGAVSSWFRQLFLAQQR

Important features:**Signal peptide:**

amino acids 1-16

Transmembrane domains:

amino acids 317-341, 451-470, 481-500, 510-527, 538-555, 831-850,
1016-1034, 1052-1070

Leucine zipper pattern.

amino acids 843-864

N-glycosylation sites.

amino acids 37-40, 268-271

FIGURE 61

TGCCGCTGCCGCCGCTGCTGCTGTTGCTCCTGGCGGCGCCTTGGGGACGGGCAGTTCCCTGT
GTCTCTGGTGGTTTGCCTAAACCTGCAAACATCACCTTCTTATCCATCAACATGAAGAATGT
CCTACAATGGACTCCACCAGAGGGTCTTCAAGGAGTTAAAGTTACTTACACTGTGCAGTATT
TCATCACAAATTGGCCCACCAGAGGTGGCACTGACTACAGATGAGAAGTCCATTTCTGTTGT
CCTGACAGCTCCAGAGAAGTGGAAGAGAAATCCAGAAGACCTTCTGTTTCCATGCAACAAA
TATACTCCAATCTGAAGTATAACGTGTCTGTGTTGAATACTAAATCAAACAGAACGTGGTCC
CAGTGTGTGACCAACCACACGCTGGTGCTCACCTGGCTGGAGCCGAACACTCTTTACTGCGT
ACACGTGGAGTCTTTCGTCCCAGGGCCCCCTCGCCGTGCTCAGCCTTCTGAGAAGCAGTGTG
CCAGGACTTTGAAAGATCAATCATCAGAGTTCAAGGCTAAAATCATCTTCTGGTATGTTTTG
CCCATATCTATTACCGTGTTTCTTTTTTCTGTGATGGGCTATTCCATCTACCGATATATCCA
CGTTGGCAAAGAGAAACACCCAGCAAATTTGATTTTGATTTATGGAAATGAATTTGACAAAA
GATTCTTTGTGCCTGCTGAAAAAATCGTGATTAACTTTATCACCTCAATATCTCGGATGAT
TCTAAAATTTCTCATCAGGATATGAGTTTACTGGGAAAAGCAGTGATGTATCCAGCCTTAA
TGATCCTCAGCCCAGCGGGAACCTGAGGCCCCCTCAGGAGGAAGAGGAGGTGAAACATTTAG
GGTATGCTTCGCATTTGATGGAAATTTTTTGTGACTCTGAAGAAAACACGGAAGGTACTTCT
CTCACCCAGCAAGAGTCCCTCAGCAGAACAAATACCCCCGGATAAAACAGTCATTGAATATGA
ATATGATGTCAGAACCACTGACATTTGTGCGGGGCTGAAGAGCAGGAGCTCAGTTTGCAGG
AGGAGGTGTCCACACAAGGAACATTATTGGAGTGCAGGCAGCGTTGGCAGTCTTGGGCCCCG
CAAACGTTACAGTACTCATAACCCCTCAGCTCCAAGACTTAGACCCCTGGCGCAGGAGCA
CACAGACTCGGAGGAGGGGCCGGAGGAAGAGCCATCGACGACCCTGGTCGACTGGGATCCCC
AAACTGGCAGGCTGTGTATTCCTTCGCTGTCCAGCTTCGACCAGGATTCAGAGGGCTGCGAG
CCTTCTGAGGGGGATGGGCTCGGAGAGGAGGGTCTTCTATCTAGACTCTATGAGGAGCCGGC
TCCAGACAGGCCACCAGGAGAAAATGAAACCTATCTCATGCAATTCATGGAGGAATGGGGGT
TATATGTGCAGATGGAAAATGATGCCAACACTTCCTTTTGCCTTTTGTTCCTGTGCAAAC
AAGTGAGTCACCCCTTTGATCCCAGCCATAAAGTACCTGGGATGAAAGAAGTTTTTCCAGT
TTGTCAGTGTCTGTGAGAATTACTTATTTCTTTTCTCTATTCTCATAGCACGTGTGTGATTG
GTTTCATGCATGTAGGTCTCTTAACAATGATGGTGGGCTCTGGAGTCCAGGGGCTGGCCGGT
TGTTCTATGCAGAGAAAGCAGTCAATAAATGTTTGCCAGACTGGGTGCAGAATTTATTCAGG
TGGGTGT

FIGURE 62

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA62815

<subunit 1 of 1, 442 aa, 1 stop

<MW: 49932, pI: 4.55, NX(S/T): 5

MSYNGLHQRVFKELKLLTLCSSISQIGPPEVALTTDEKSISVVLTAPEKWKRNPEDLPVSMQ
QIYSNLKYNVSVLNTKSNRTWSQCVTNHTLVLTWLEPNTLYCVHVESFVPGPPRAQPSEKQ
CARTLKDQSSEFKAKIIFWYVLPISITVFLFSVMGYSIYRYIHVGKEKHPANLILYGNEDF
KRFFVPAEKIVINFITLNISDDSKISHQDMSLLGKSSDVSSLNDPQPSGNLRPPQEEEEVKH
LGYASHLMEIFCDSEENTEGTSLTQQESLSRTIPDKTVIEYDYVRTTDICAGPEEQELSL
QEEVSTQGTLLESQAALAVLGPQTLQYSYTPQLQDLPLAQEHTDSEEGPEEEPSTTLVDWD
PQTGRLCIPSLSSFDQDSEGCEPSEGDLGEEGLLSRLYEAPAPDRPPGENETYLMQFMEEW
GLYVQMEN

Important features:**Signal peptide:**

amino acids 1-28

Transmembrane domain:

amino acids 140-163

N-glycosylation sites.

amino acids 71-74, 80-83, 89-92, 204-207, 423-426

FIGURE 63

CGGACGCGTGGGCGGACGCGTGGGCGGACGCGTGGGTCTCTGCGGGGAGACGCCAGCCTGCG
TCTGCCATGGGGCTCGGGTTGAGGGGCTGGGGACGTCTCTGCTGACTGTGGCCACCGCCCT
GATGCTGCCCCGTGAAGCCCCCGCAGGCTCCTGGGGGGCCAGATCATCGGGGGCCACGAGG
TGACCCCCCACTCCAGGCCCTACATGGCATCCGTGCGCTTCGGGGGCCAACATCACTGCGGA
GGCTTCCTGCTGCGAGCCCGCTGGGTGGTCTCGGCCGCCCACTGCTTCAGCCACAGAGACCT
CCGCACTGGCCTGGTGGTGTGCTGGGCGCCACGTCTGAGTACTGCGGAGCCACCCAGCAGG
TGTTTGGCATCGATGCTCTCACCACGCACCCCGACTACCACCCCATGACCCACGCCAACGAC
ATCTGCCTGCTGCGGCTGAACGGCTCTGCTGTCTGCTGGGCCCTGCAGTGGGGCTGCTGAGGCT
GCCAGGGAGAAGGGCCAGGCCCCCACAGCGGGGACACGGTGCCGGGTGGCTGGCTGGGGCT
TCGTGTCTGACTTTGAGGAGCTGCCGCCTGGACTGATGGAGGCCAAGGTCCGAGTGCTGGAC
CCGGACGTCTGCAACAGCTCCTGGAAGGGCCACCTGACACTTACCATGCTCTGCACCCGCAG
TGGGGACAGCCACAGACGGGGCTTCTGCTCGGCCGACTCCGGAGGGCCCCCTGGTGTGCAGGA
ACCGGGCTCACGGCCTCGTTTCCTTCTCGGGCCTCTGGTGCGGCGACCCCAAGACCCCGAC
GTGTACACGCAGGTGTCCGCCTTTGTGGCCTGGATCTGGGACGTGGTTCCGGCGGAGCAGTCC
CCAGCCCGGCCCCCTGCCTGGGACCACCAGGCCCCCAGGAGAAGCCGCCTTGAGCCACAACCT
TGCGGCATGCAAATGAGATGGCCGCTCCAGGCCTGGAATGTTCCGTGGCTGGGCCCCACGGG
AAGCCTGATGTTTCAAGGTTGGGGTGGGACGGGCAGCGGTGGGGCACACCCATTCCACATGCA
AAGGGCAGAAGCAAACCCAGTAAAATGTTAAGTACAAAAAAAAAAAAAAAAAAAAAGAAA

FIGURE 64

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA62845

><subunit 1 of 1, 283 aa, 1 stop

><MW: 30350, pI: 9.66, NX(S/T): 2

MGLGLRGWGRPLLTVATALMLPVKPPAGSWGAIIGGHEVTPHSRPYMASVRFGGQHHCGGF
LLRARWVVSAAHCFSHRDLRTGLVVLGAHVLSTAEP TQQVFGIDALTTHPDYHPMTHANDIC
LLRLNGSAVLGPAVGLLRLPGRRARPPTAGTRCRVAGWGFVSDFEELPPGLMEAKVRVLDPD
VCNSSWKGHLTLTMLCTRSGDSHRRGFCSADSGGPLVCRNRAHGLVSFSGLWCGDPKTPDVY
TQVSAFVAWIWDVVRSSPQPGPLPGTTTRPPGEAA

Signal peptide:

amino acids 1-30

64/270

FIGURE 65

GAGCTACCCAGGCGGCTGGTGTGCAGCAAGCTCCGCGCCGACTCCGGACGCCTGACGCCTGA
CGCCTGTCCCCGGCCCCGGCATGAGCCGCTACCTGCTGCCGCTGTCGGCGCTGGGCACGGTAG
CAGGCGCCGCGCTGCTGCTCAAGGACTATGTCACCGGTGGGGCTTGCCCCAGCAAGGCCACC
ATCCCTGGGAAGACGGTCATCGTGACGGGCGCCAACACAGGCATCGGGAAGCAGACCGCCTT
GGAAGTGGCCAGGAGAGGAGGCAACATCATCCTGGCCTGCCGAGACATGGAGAAGTGTGAGG
CGGCAGCAAAGGACATCCGCGGGGAGACCCTCAATCACCATGTCAACGCCCGGCACCTGGAC
TTGGCTTCCCTCAAGTCTATCCGAGAGTTTGCAGCAAAGATCATTGAAGAGGAGGAGCGAGT
GGACATTCTAATCAACAACGCGGGTGTGATGCGGTGCCCCACTGGACCACCGAGGACGGCT
TCGAGATGCAGTTTGGCGTTAACCACCTGGGTCACTTCTCTTGACAACTTGCTGCTGGAC
AAGCTGAAAGCCTCAGCCCCCTCGCGGATCATCAACCTCTCGTCCCTGGCCCATGTTGCTGG
GCACATAGACTTTGACGACTTGAAGTGGCAGACGAGGAAGTATAACACCAAAGCCGCCTACT
GCCAGAGCAAGCTCGCCATCGTCCTCTTCACCAAGGAGCTGAGCCGGCGGCTGCAAGGCTCT
GGTGTGACTGTCAACGCCCTGCACCCCGGCGTGGCCAGGACAGAGCTGGGCAGACACACGGG
CATCCATGGCTCCACCTTCTCCAGCACCACACTCGGGCCCATCTTCTGGCTGCTGGTCAAGA
GCCCCGAGCTGGCCGCCAGCCAGCACATACCTGGCCGTGGCGGAGGAAGTGGCGGATGTT
TCCGGAAAGTACTTCGATGGACTCAAACAGAAGGCCCGGCCCGAGGCTGAGGATGAGGA
GGTGGCCCGGAGGCTTTGGGCTGAAAGTGCCCGCCTGGTGGGCTTAGAGGCTCCCTCTGTGA
GGGAGCAGCCCCCTCCCCAGATAAACCTCTGGAGCAGATTTGAAAGCCAGGATGGCGCCTCCAG
ACCGAGGACAGCTGTCCGCCATGCCCGCAGCTTCTGGCACTACCTGAGCCGGGAGACCCAG
GACTGGCGGCCCGCCATGCCCGCAGTAGGTTCTAGGGGGCGGTGCTGGCCGCAGTGGACTGGC
CTGCAGGTGAGCACTGCCCCGGGCTCTGGCTGGTTCCGTCTGCTCTGCTGCCAGCAGGGGAG
AGGGGCCATCTGATGCTTCCCCTGGGAATCTAAACTGGGAATGGCCGAGGAGGAAGGGGCTC
TGTGCACTTGCAGGCCACGTCAGGAGAGCCAGCGGTGCCTGTGCGGGAGGGTTCCAAGGTGC
TCCGTGAAGAGCATGGGCAAGTTGTCTGACACTTGGTGGATTCTTGGGTCCCTGTGGGACCT
TGTGCATGCATGGTCCTCTCTGAGCCTTGGTTTCTTCAGCAGTGAGATGCTCAGAATAACTG
CTGTCTCCCATGATGGTGTGGTACAGCGAGCTGTTGTCTGGCTATGGCATGGCTGTGCCGGG
GGTGTGTTGCTGAGGGCTTCTGTGCCAGAGCCAGCCAGAGAGCAGGTGCAGGTGTCATCCC
GAGTTCAGGCTCTGCACGGCATGGAGTGGGAACCCACCAGCTGCTGCTACAGGACCTGGGA
TTGCCTGGGACTCCACCTTCTATCAATTCTCATGGTAGTCCAAACTGCAGACTCTCAAAC
TTGCTCATTT

FIGURE 66

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64842

><subunit 1 of 1, 331 aa, 1 stop

><MW: 35932, pI: 8.45, NX(S/T): 1

MSRYLLPLSALGTVAGAAVLLKDYVTGGACPSKATIPGKTIVITGANTGIGKQTALELARRG
GNIILACRDMEKCEAAAKDIRGETLNHHVNARHLDLASLKSIREFAAKIIEEEERV DILINN
AGVMRCPHWTTEDGFEMQFGVNHLGHFLLTNLLLDKLGKASAPSRIINLSSLAHVAGHIDFDD
LNWQTRKYNTKAAYCQSKLAIVLFTKELSRRLQSGVTVNALHPGVARTELGRHTGIHGSTF
SSTTLGPFIWLLVKSPELAAQPSTYLAVAEELADVSGKYFDGLKQKAPAPEAEDEEVARRLW
AESARLVGLEAPSVREQPLPR

Signal peptide:

amino acids 1-17

66/270

FIGURE 67

GAAGTTCGCGAGCGCTGGCATGTGGTCCTGGGGCGCGGCTGGCGGCGCTGCTGGCGGTGCTG
GCGCTCGGGACAGGAGACCCAGAAAGGGCTGCGGCTCGGGGCGACACGTTCTCGGCGCTGAC
CAGCGTGGCGCGCGCCCTGGCGCCCCGAGCGCCGGCTGCTGGGGCTGCTGAGGCGGTACCTGC
GCGGGGAGGAGGCGCGGCTGCGGGACCTGACTAGATTCTACGACAAGGTACTTTCTTTGCAT
GAGGATTCAACAACCCCTGTGGCTAACCCCTGCTTGCATTTACTCTCATCAAACGCCTGCA
GTCTGACTGGAGGAATGTGGTACATAGTCTGGAGGCCAGTGAGAACATCCGAGCTCTGAAGG
ATGGCTATGAGAAGGTGGAGCAAGACCTTCCAGCCTTTGAGGACCTTGAGGGAGCAGCAAGG
GCCCTGATGCGGCTGCAGGACGTGTACATGCTCAATGTGAAAGGCCTGGCCCCGAGGTGTCTT
TCAGAGAGTCACTGGCTCTGCCATCACTGACCTGTACAGCCCCAAACGGCTCTTTTCTCTCA
CAGGGGATGACTGCTTCCAAGTTGGCAAGGTGGCCTATGACATGGGGGATTATTACCATGCC
ATTCCATGGCTGGAGGAGGCTGTGAGTCTCTTCCGAGGATCTTACGGAGAGTGGAAGACAGA
GGATGAGGCAAGTCTAGAAGATGCCTTGGATCACTTGGCCTTTGCTTATTTCCGGGCAGGAA
ATGTTTCGTGTGCCCTCAGCCTCTCTCGGGAGTTTCTTCTCTACAGCCCAGATAATAAGAGG
ATGGCCAGGAATGTCTTGAAATATGAAAGGCTCTTGGCAGAGAGCCCCAACACGTGGTAGC
TGAGGCTGTCTATCCAGAGGCCCAATATACCCACCTGCAGACCAGAGACACCTACGAGGGGC
TATGTGAGACCCTGGGTTCCCAGCCCACTCTCTACCAGATCCCTAGCCTCTACTGTTCCCTAT
GAGACCAATTCCAACGCCTACCTGCTGCTCCAGCCCATCCGGAAGGAGGTCTACACCTGGA
GCCCTACATTGCTCTCTACCATGACTTCGTGAGTCACTCAGAGGCTCAGAAAATTAGAGAAC
TTGCAGAACCATGGCTACAGAGGTGAGTGGTGGCATCAGGGGAGAAGCAGTTACAAGTGGAG
TACCGCATCAGCAAAAGTGCCTGGCTGAAGGACACTGTTGACCCAAAACCTGGTGACCCCTCAA
CCACCGCATTGCTGCCCTCACAGGCCTTGATGTCCGGCCTCCCTATGCAGAGTATCTGCAGG
TGGTGAACATATGGCATCGGAGGACACTATGAGCCTCACTTTGACCATGCTACGTCACCAAGC
AGCCCCCTCTACAGAATGAAGTCAGGAAACCGAGTTGCAACATTTATGATCTATCTGAGCTC
GGTGAAGCTGGAGGAGCCACAGCCTTCATCTATGCCAACCTCAGCGTGCCTGTGGTTAGGA
ATGCAGCACTGTTTTGGTGGAACTTGCACAGGAGTGGTGAAGGGGACAGTGACACACTTCAT
GCTGGCTGTCTGTCTGCTGGTGGGAGATAAGTGGGTGGCCAACAAGTGGATACATGAGTATGG
ACAGGAATTCCGCAGACCCTGCAGCTCCAGCCCTGAAGACTGAACCTGTTGGCAGAGAGAAGC
TGGTGGAGTCTGTGGCTTTCCAGAGAAGCCAGGAGCCAAAAGCTGGGGTAGGAGAGGAGAA
AGCAGAGCAGCCTCCTGGAAGAAGGCCTTGTGAGCTTTGTCTGTGCCTCGCAATCAGAGGC
AAGGGAGAGGTTGTTACCAGGGGACACTGAGAATGTACATTTGATCTGCCCCAGCCACGGAA
GTCAGAGTAGGATGCACAGTACAAAGGAGGGGGGAGTGGAGGCCTGAGAGGGAAGTTTCTGG
AGTTCAGATACTCTCTGTTGGGAACAGGACATCTCAACAGTCTCAGGTTGATCAGTGGGTCT
TTTTGGCACTTTGAACCTTGACCACAGGGACCAAGAAGTGGCAATGAGGACACCTGCAGGAG
GGGCTAGCCTGACTCCAGAACTTTAAGACTTTCTCCCCACTGCCTTCTGCTGCAGCCCAAG
CAGGGAGTGTCCCCCTCCAGAAAGCATATCCAGATGAGTGGTACATTATATAAGGATTTTT
TTTAAAGTTGAAAACAACCTTTCTTTTCTTTTTGTATGATGGTTTTTTAACACAGTCATTAAAA
ATGTTTATAAATCAAAA

FIGURE 68

MGPGARLAALLAVLALGTGDPERAAARGDTFSALTSVARALAPERLLGLLRRYLRGEEARL
RDLTRFYDKVLSLHEDSTTPVANPLLAFTLIKRLQSDWRNVVHSLEASENIRALKDGYEKVE
QDLPAFEDLEGAARALMRLQDVYMLNVKGLARGVFQRTGSAITDLYSPKRLFSLTGDDCFQ
VGKVAYDMGDYYHAIPWLEEAVSLFRGSYGEWKTEDEASLEDALDHLAFAYFRAGNVSCALS
LSREFLLYSPDNKRMARNVLKYERLLAESPNHVVAEAVIQRPNIPHLQTRDTYEGLCQTLGS
QPTLYQIPSLYCSYETNSNAYLLLQPIRKEVIHLEPYIALYHDFVSDSEAQKIRELAEPWLQ
RSVVASGEKQLQVEYRISKSAWLKDTVDPKLVTLNHRIAALTGLDVRPPYAEYLQVVNYGIG
GHYEPHFDHATSPSSPLYRMKSGNRVATFMIYLSSVEAGGATAFIYANLSVPVVRNAALFWW
NLHRSGEGDSDTLHAGCPVLVGDKWVANKWIHEYGQEFRRPCSSSPED

Signal peptide:

amino acids 1-19

FIGURE 69

GAGATAGGGAGTCTGGGTTTAAAGTTCCTGCTCCATCTCAGGAGCCCCTGCTCCCACCCCTAG
GAAGCCACCAGACTCCACGGTGTGGGGCCAATCAGGTGGAATCGGCCCTGGCAGGTGGGGCC
ACGAGCGCTGGCTGAGGGACCGAGCCGGAGAGCCCCGGAGCCCCCGTAACCCGCGCGGGGAG
CGCCCAGGATGCCGCGCGGGGACTCGGAGCAGGTGCGCTACTGCGCGCGCTTCTCCTACCTC
TGGCTCAAGTTTTCACTTATCATCTATTCCACCGTGTCTGGCTGATTGGGGCCCTGGTCCT
GTCTGTGGGCATCTATGCAGAGGTTGAGCGGCAGAAATATAAAACCCTTGAAAGTGCCTTCC
TGGCTCCAGCCATCATCCTCATCCTCCTGGGCGTCGTCATGTTTCATGGTCTCCTTCATTGGT
GTGCTGGCGTCCCTCCGTGACAACCTGTACCTTCTCCAAGCATTTCATGTACATCCTTGGGAT
CTGCCTCATCATGGAGCTCATTGGTGGCGTGGTGGCCTTGACCTTCCGGAACCAGACCATTG
ACTTCCTGAACGACAACATTCTGAAGAGGAATTGAGAACTACTATGATGATCTGGACTTCAAA
AACATCATGGACTTTGTTTCAGAAAAAGTTCAAGTGCTGTGGCGGGGAGGACTACCGAGATTG
GAGCAAGAATCAGTACCACGACTGCAGTGCCCCCTGGACCCCTGGCCTGTGGGGTGCCCTACA
CCTGCTGCATCAGGAACACGACAGAAGTTGTCAACACCATGTGTGGCTACAAACTATCGAC
AAGGAGCGTTTCAGTGTGCAGGATGTCTACGTGCGGGGCTGCACCAACGCCGTGATCAT
CTGGTTCATGGACAACTACACCATCATGGCGTGCATCCTCCTGGGCATCCTGCTTCCCCAGT
TCCTGGGGGTGCTGCTGACGCTGCTGTACATCACCCGGGTGGAGGACATCATCATGGAGCAC
TCTGTCACTGATGGGCTCCTGGGGCCCCGGTGCCAAGCCCAGCGTGGAGGCGGCAGGCACGGG
ATGCTGCTTGTGCTACCCCAATTAGGGCCCAGCCTGCCATGGCAGCTCCAACAAGGACCGTC
TGGGATAGCACCTCTCAGTCAACATCGTGGGGCTGGACAGGGCTGCGGCCCTCTGCCCACA
CTCAGTACTGACCAAAGCCAGGGCTGTGTGTGCCTGTGTGTAGGTCCCACGGCCTCTGCCTC
CCCAGGGAGCAGAGCCTGGGCCTCCCCTAAGAGGCTTTCCCCGAGGCAGCTCTGGAATCTGT
GCCACCTGGGGCCTGGGGAACAAGGCCCTCCTTTCTCCAGGCCTGGGCTACAGGGGAGGGA
GAGCCTGAGGCTCTGCTCAGGGCCCATTTTCATCTCTGGCAGTGCCTTGGCGGTGGTATTCAA
GGCAGTTTTGTAGCACCTGTAATTGGGGAGAGGGAGTGTGCCCTCGGGGCAGGAGGGAAGG
GCATCTGGGGAAGGGCAGGAGGGAAGAGCTGTCCATGCAGCCACGCCCATGGCCAGGTGGC
CTCTTCTCAGCCTCCCAGGTGCCTTGAGCCCTCTTGCAAGGGCGGCTGCTTCCTTGAGCCTA
GTTTTTTTTTACGTGATTTTTGTAAACATTCATTTTTTTGTACAGATAACAGGAGTTTCTGAC
TAATCAAAGCTGGTATTTCCCCGCATGTCTTATTCTTGCCCTTCCCCCAACCAGTTTGTAA
TCAAACAATAAAAAACATGTTTTGTTTTGTTTTTAAAAAAA

FIGURE 70

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64863

><subunit 1 of 1, 294 aa, 1 stop

><MW: 33211, pI: 5.35, NX(S/T): 3

MPRGDSEQVRYCARFSYLWLKFSLLIYSTVFWLIGALVLSVGIYAEVERQKYKTLES AFLAP
AAILILLGVVMFMVSFIGVLASLRDNLVLLQAFMYILGICLIMELIGGVVALTFRNQ TIDFL
NDNIRRGIE NYDDLD FKNIMDFVQKKFKCCGGEDYRDWSKNQYHDCSAPG PLACGV PYTCC
IRNTTEVVNTMCGYKTIDKERFSVQDVIYVRGCTNAVI IWFMDNYTIMACILLGILLPQFLG
VLLTLLYITRVEDI IMEHSVTDG LLGPGAKPSVEAAGTGCCLCYPN

Signal peptide:

amino acids 1-44

Transmembrane domains:

amino acids 22-42, 57-85, 93-116, 230-257

70/270

FIGURE 71

GAGGAGCGGGCCGAGGACTCCAGCGTGCCAGGTCTGGCATCCTGCACTTGCTGCCCTCTGA
CACCTGGGAAGATGGCCGGCCCGTGGACCTTCACCCTTCTCTGTGGTTTGCTGGCAGCCACC
TTGATCCAAGCCACCCTCAGTCCCAGTTCATCCTCGGCCAAAAGTCATCAAAGA
AAAGCTGACACAGGAGCTGAAGGACCACAACGCCACCAGCATCCTGCAGCAGCTGCCGCTGC
TCAGTGCCATGCGGGAAAAGCCAGCCGGAGGCATCCCTGTGCTGGGCAGCCTGGTGAACACC
GTCCTGAAGCACATCATCTGGCTGAAGGTCATCACAGCTAACATCCTCCAGCTGCAGGTGAA
GCCCTCGGCCAATGACCAGGAGCTGCTAGTCAAGATCCCCCTGGACATGGTGGCTGGATTCA
ACACGCCCCCTGGTCAAGACCATCGTGGAGTTCCACATGACGACTGAGGCCAAGCCACCATC
CGCATGGACACCAGTGCAAGTGGCCCCACCCGCTGGTCTCAGTGAAGTGTGCCACCAGCCA
TGGGAGCCTGCGCATCCAAGTGTGTATAAGCTCTCCTTCCTGGTGAACGCCTTAGCTAAGC
AGGTCATGAACCTCCTAGTGCCATCCCTGCCCAATCTAGTGAAAAACCAGCTGTGTCCCGTG
ATCGAGGCTTCCTTCAATGGCATGTATGCAGACCTCCTGCAGCTGGTGAAGGTGCCATTTC
CCTCAGCATTGACCGTCTGGAGTTTGACCTTCTGTATCCTGCCATCAAGGGTGACACCATTC
AGCTCTACCTGGGGGCCAAGTTGTTGGACTCACAGGGAAAGGTGACCAAGTGGTTCAATAAC
TCTGCAGCTTCCTGACAATGCCACCCTGGACAACATCCCGTTCAGCCTCATCGTGAGTCA
GGACGTGGTGAAGCTGCAGTGGCTGCTGTGCTCTCTCCAGAAGAATTATGGTCCTGTTGG
ACTCTGTGCTTCCTGAGAGTGCCCATCGGCTGAAGTCAAGCATCGGGCTGATCAATGAAAAG
GCTGCAGATAAGCTGGGATCTACCCAGATCGTGAAGATCCTAACTCAGGACACTCCCGAGTT
TTTTATAGACCAAGGCCATGCCAAGGTGGCCCAACTGATCGTGCTGGAAGTGTTTCCCTCCA
GTGAAGCCCTCCGCCCTTTGTTTACCCTGGGCATCGAAGCCAGCTCGGAAGCTCAGTTTTAC
ACCAAAGGTGACCAACTTATACTCAACTTGAATAACATCAGCTCTGATCGGATCCAGCTGAT
GAACTCTGGGATTGGCTGGTTCCAACCTGATGTTCTGAAAAACATCATCACTGAGATCATCC
ACTCCATCCTGCTGCCGAACCAGAATGGCAAATTAAGATCTGGGGTCCCAGTGTGATTGGTG
AAGGCCTTGGGATTCGAGGCAGCTGAGTCCTCACTGACCAAGGATGCCCTTGTGCTTACTCC
AGCCTCCTTGTGGAAACCCAGCTCTCCTGTCTCCAGTGAAGACTTGGATGGCAGCCATCAG
GGAAGGCTGGGTCCCAGCTGGGAGTATGGGTGTGAGCTCTATAGACCATCCCTCTCTGCAAT
CAATAAACACTTGCCTGTGAAAAA

FIGURE 72

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64881

><subunit 1 of 1, 484 aa, 1 stop

><MW: 52468, pI: 7.14, NX(S/T): 3

MAGPWTFTLLCGLLAATLIQATLSPTAVLILGPKVIKEKLTQELKDHNATSILQQLPLLSAM
REKPAGGIPVLGSLVNTVLKHIIWLKVITANILQLQVKPSANDQELLVKIPLDMVAGFNTPL
VKTIVEFHMTTEAQATIRMDTSASGPTRLVLSDCATSHGSLRIQLLYKLSFLVNALAKQVMN
LLVPSLPNLVKNQLCPVIEASFNGMYADLLQLVKVPISLSIDRLEFDLLYPAIKGDTIQLYL
GAKLLDSQGKVTWKFNNNSAASLTMPITLDNIPFSLIVSQDVVKAAVAVALSPEEFMVLLDSVL
PESAHRLKSSIGLINEKAADKLGSTQIVKILTQDTPEFFIDQGHAKVAQLIVLEVFPSSSEAL
RPLFTLGIEASSEAQFYTKGDQLILNLNLISSDRIQLMNSGIGWFQPDVLKNIITEIIHSIL
LPNQNGKLRSQVPVSLVKALGFEEAESSLTkdALVLTpASLWKPSSPVSQ

Important features of the protein:

Signal peptide:

amino acids 1-21

N-glycosylation sites.

amino acids 48-51, 264-267, 401-404

Glycosaminoglycan attachment site.

amino acids 412-415

LBP / BPI / CETP family proteins.

amino acids 407-457

FIGURE 73

GAGCGAACATGGCAGCGCGTTGGCGGTTTTGGTGTGTCTCTGTGACCATGGTGGTGGCGCTG
CTCATCGTTTTGCGACGTTCCCTCAGCCTCTGCCCCAAAGAAAGAAGGAGATGGTGTATCTGA
AAAGGTTAGTCAGCTGATGGAATGGACTAACAAAAGACCTGTAATAAGAATGAATGGAGACA
AGTTCCGTCGCTTGTGAAAGCCCCACCGAGAAATTACTCCGTTATCGTCATGTTCACTGCT
CTCCAACCTGCATAGACAGTGTGTCTTTTTGCAAGCAAGCTGATGAAGAATTCCAGATCCTGGC
AAACTCCTGGCGATACTCCAGTGCATTACCAACAGGATATTTTTTGCCATGGTGGATTTTG
ATGAAGGCTCTGATGTATTTAGATGCTAAACATGAATTCAGCTCCAACCTTTCATCAACTTT
CCTGCAAAAGGGAAACCCAAACGGGGTGATACATATGAGTTACAGGTGCGGGGTTTTTCAGC
TGAGCAGATTGCCCCGGTGGATCGCCGACAGAACTGATGTCAATATTAGAGTGATTAGACCCC
CAAATTATGCTGGTCCCCTTATGTTGGGATTGCTTTTGGCTGTTATTGGTGGACTTGTGTAT
CTTCGAAGAAGTAATATGGAATTTCTCTTTAATAAAACTGGATGGGCTTTTGCAGCTTTGTG
TTTTGTGCTTGCTATGACATCTGGTCAAATGTGGAACCATATAAGAGGACCACCATATGCCC
ATAAGAATCCCCACACGGGACATGTGAATTATATCCATGGAAGCAGTCAAGCCCAGTTTGTA
GCTGAAACACACATTGTTCTTCTGTTTAAATGGTGGAGTTACCTTAGGAATGGTGTCTTTATG
TGAAGCTGCTACCTCTGACATGGATATTGGAAGCGAAAGATAATGTGTGTGGCTGGTATTG
GACTTGTTGTATTATTCTTCAGTTGGATGCTCTCTATTTTTAGATCTAAATATCATGGCTAC
CCATACAGCTTTCTGATGAGTTAAAAAGGTCCCAGAGATATATAGACACTGGAGTACTGGAA
ATTGAAAAACGAAATCGTGTGTGTTTGAAAAGAAGAATGCAACTTGTATATTTTGTATTAC
CTCTTTTTTTCAAGTGATTTAAATAGTTAATCATTTAACCAGAAAGATGTGTAGTGCCTTA
ACAAGCAATCCTCTGTCAAAATCTGAGGTATTTGAAAATAATTATCCTCTTAACCTTCTCTT
CCCAGTGAACCTTTATGGAACATTTAATTTAGTACAATTAAGTATATTATAAAAATTGTAAAA
CTACTACTTTGTTTTTAGTTAGAACAAAGCTCAAACTACTTTAGTTAACTTGGTCATCTGAT
TTTATATTGCCTTATCCAAAGATGGGGAAAGTAAGTCCTGACCAGGTGTTCCACATATGCC
TGTTACAGATAACTACATTAGGAATTCATTCTTAGCTTCTTCATCTTTGTGTGGATGTGTAT
ACTTTACGCATCTTTCCTTTTGAGTAGAGAAATTATGTGTGTGATGTGGTCTTCTGAAAATG
GAACACCATTCTTCAGAGCACACGTCTAGCCCTCAGCAAGACAGTTGTTTCTCCTCCTCCTT
GCATATTTCTACTGCGCTCCAGCCTGAGTGATAGAGTGAGACTCTGTCTCAAAAAAAGTA
TCTCTAAATACAGGATTATAATTTCTGCTTGAGTATGGTGTAACTACCTTGATTTAGAAA
GATTTAGATTCAATCCATCTCCTTAGTTTTCTTTAAGGTGACCCATCTGTGATAAAAATA
TAGCTTAGTGCTAAAATCAGTGTAACCTTATACATGGCCTAAAATGTTTCTACAAATTAGAGT
TTGTCACTTATTCCATTTGTACCTAAGAGAAAAATAGGCTCAGTTAGAAAAGGACTCCCTGG
CCAGGCGCAGTGACTTACGCCTGTAATCTCAGCACTTTGGGAGGCCAAGGCAGGCAGATCAC
GAGGTGAGGAGTTCGAGACCATCCTGGCCAACATGGTGAAACCCCGTCTCTACTAAAAATAT
AAAAATTAGCTGGGTGTGGTGGCAGGAGCCTGTAATCCCAGCTACACAGGAGGCTGAGGCAC
GAGAATCACTTGAACCTCAGGAGATGGAGGTTTTAGTGAGCCGAGATCACGCCACTGCACTCC
AGCCTGGCAACAGAGCGAGACTCCATCTCAAAAAAAAAAAAAA

FIGURE 74

MAARWRFWCVSVTMVVALLI VCDVPSASAQRKKEMVLSEKVSQ LMEWTNKR PVIRMNGDKFR
RLVKAPPRNYSVIVMFTALQLHRQCVVCKQADEEFQILANSWRYSSAFTNRIFFAMVDFDEG
SDVFQMLNMNSAPTFINFPAKGKPKRGDTYELQVRGFSAEQIARWIADRTDVNIRVIRPPNY
AGPLMLGLLLAVIGGLVYLRRSNMEFLFNKTGWAFALCFVLAMTSGQMWNHIRGPPYAHKN
PHTGHVNYIHGSSQAQFVAETHIVLLFNGGVT LGMVLLCEAATSDMDIGKRKIMCVAGIGLV
VLFFSWMLSIFRSKYHGYPSFLMS

Signal peptide:

amino acids 1-29

Transmembrane domains:

amino acids 183-205, 217-237, 217-287, 301-321

FIGURE 75

AAGCAACCAAAGCTGCAAGCTTTGGGAGTTGTTGCTGTCCCTGCCCTGCTCTGCTAGGGAGA
GAACGCCAGAGGGAGGCGGCTGGCCCGGCGGCAGGCTCTCAGAACCCTACCGGCGATGCTA
CTGCTGTGGGTGTGCGGTGGTCGACGCTTGGCGCTGGCGGTACTGGCCCCGGAGCAGGGGA
GCAGAGGCGGAGAGCAGCCAAAGCGCCCAATGTGGTGCTGGTCGTGAGCGACTCCTTCGATG
GAAGGTTAACATTTTCATCCAGGAAGTCAGGTAGTGAAACTTCCTTTTATCAACTTTATGAAG
ACACGTGGGACTTCCTTTCTGAATGCCTACACAACTCTCCAATTTGTTGCCCATCACGCGC
AGCAATGTGGAGTGGCCTCTTCACTCACTTAACAGAATCTTGAATAATTTTAAGGGTCTAG
ATCCAAATTATACAACATGGATGGATGTCATGGAGAGGCATGGCTACCGAACACAGAAATTT
GGGAACTGGACTATACTTCAGGACATCACTCCATTAGTAATCGTGTGGAAGCGTGGACAAG
AGATGTTGCTTTCTTACTCAGACAAGAAGGCAGGCCCATGGTTAATCTTATCCGTAACAGGA
CTAAAGTCAGAGTGATGGAAGGGATTGGCAGAATACAGACAAAGCAGTAACTGGTTAAGA
AAGGAAGCAATTAATTACACTGAACCATTTGTTATTTACTTGGGATTAATTTTACCACACCC
TTACCCTTCACCATCTTCTGGAGAAAAATTTGGATCTTCAACATTTACACATCTCTTTATT
GGCTTGAAAAGTGTCTCATGATGCCATCAAAATCCCAAAGTGGTCACCTTTGTGAGAAATG
CACCTGTAGATTATTACTCTTCTTATACAAAAAAGTGCCTGGAGATTTACAAAAGGA
AATTAAGAATATTAGAGCATTTTATTATGCTATGTGTGCTGAGACAGATGCCATGCTTGGTG
AAATTATTTTGGCCCTTCATCAATTAGATCTTCTTCAGAAAACTATTGTATATACTCCTCA
GACCATGGAGAGCTGGCCATGGAACATCGACAGTTTATAAAATGAGCATGTACGAGGCTAG
TGCACATGTTCCGCTTTTGATGATGGGACCAGGAATTAAGCCGGCCTACAAGTATCAAATG
TGGTTTCTCTTGTGGATATTTACCCTACCATGCTTGATATTGCTGGAATTCCTCTGCCTCAG
AACCTGAGTGGATACTCTTTGTTGCCGTATCATCAGAAACATTTAAGAATGAACATAAAGT
CAAAAACCTGCATCCACCCTGGATTCTGAGTGAATTCATGGATGTAATGTGAATGCCTCCA
CCTACATGCTTCGAACTAACCCTGGAAATATATAGCCTATTCCGATGGTGCATCAATATTG
CCTCAACTCTTTGATCTTTCCTCGGATCCAGATGAATTAACAAATGTTGCTGTAAAATTTCC
AGAAATTACTTATTCTTTGGATCAGAAGCTTCATTCCATTATAAACTACCCTAAAGTTTCTG
CTTCTGTCCACCAGTATAATAAAGAGCAGTTTATCAAGTGGAAACAAAGTATAGGACAGAAT
TATTCAAACGTTATAGCAAATCTTAGGTGGCACCAGACTGGCAGAAGGAACCAAGGAAGTA
TGAAAATGCAATTGATCAGTGGCTTAAACCCATATGAATCCAAGAGCAGTTTGAACAAAAA
GTTTAAAAATAGTGTTCTAGAGATACATATAAATATATTACAAGATCATAATTATGTATTTT
AAATGAAACAGTTTAAATAATTACCAAGTTTGGCCGGGCACAGTGGCTCACACCTGTAATC
CCAGGACTTTGGGAGGCTGAGGAAAGCAGATCACAAGGTCAAGAGATTGAGACCATCCTGGC
CAACATGGTGAAACCCTGTCTCTACTAAAAATACAAAAATTAGCTGGGCGCGGTGGTGACA
CCTATAGTCTCAGCTACTCAGAGGCTGAGGCAGGAGGATCGCTTGAACCCGGGAGGCAGCAG
TTGCAGTGAGCTGAGATTGCGCCACTGTACTCCAGCCTGGCAACAGAGTGAGACTGTGTGCG
AAAAAATAAAAAATAAATAAATAATTACCAATTTTTCATTATTTTGAAGAATGTAGTG
TATTTTAAGATAAAATGCCAATGATTATAAAATCACATATTTTCAAAAATGGTTATTATTTA
GGCCTTTGTACAATTTCTAACAATTTAGTGGAAGTATCAAAAGGATTGAAGCAAATACTGTA
ACAGTTATGTTCCCTTTAAATAATAGAGAATATAAAATATTGTAATAATATGTATCATAAAT
AGTTGTATGTGAGCATTTGATGGTGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
AAA

FIGURE 76

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64885
<subunit 1 of 1, 536 aa, 1 stop
<MW: 61450, pI: 9.17, NX(S/T): 7
MLLLWVSVVAALALAVLAPGAGEQRRRAAKAPNVVLVVSDFSFGRLTFHPGSQVVKLPFINF
MKTRGTSFLNAYTNSPICCPSSRAAMWSGLFTHLTESWNNFKGLDPNYTTWMDVMERHGYRTQ
KFGKLDYTSGHHSISNRVEAWTRDVAFLLRQEGRPVMNLRNRTKVRVMERDQNTDKAVNW
LRKEAINYTEPFVIYLG LNLPHYPSPSSGENFGSSSTFHTSLYWLEKVS HDAIKIPKWSPLS
EMHPVDYYSYTKNCTGRFTKKEIKNIRAFYYAMCAETDAMLGEIILALHQLDLLQKTIVIIY
SSDHGELAMEHRQFYKMSMYEASAHVPLMMGPGIKAGLQVSNVSLVDIYPTMLDIAGIPL
PQNLSGYSLPLSSETFKNEHKVKNLHPPWILSEFHGCNVNASTYMLRTNHWKYIAYSDGAS
ILPQLFDLSSDPDEL TNVAVKFPEITYSLDQKLHSIINYPKVSASVHQYNKEQFIKWKQSIG
QNYSNVIANLRWHQDWQKEPRKYENAI DQWLKTHMNPRAV

Important features:**Signal peptide:**

amino acids 1-15

N-glycosylation sites.amino acids 108-111, 166-169, 193-196, 262-265, 375-378, 413-416,
498-501**Sulfatases proteins:**

amino acids 286-315, 359-369, 78-97

76/270

FIGURE 77

GAGAGAAGTCAGCCTGGCAGAGAGACTCTGAAATGAGGGATTAGAGGTGTTCAAGGAGCAAG
AGCTTCAGCCTGAAGACAAGGGAGCAGTCCCTGAAGACGCTTCTACTGAGAGGTCTGCCATG
GCCTCTCTTGGCCTCCAACTTGTGGGCTACATCCTAGGCCTTCTGGGGCTTTTGGGCACACT
GGTTGCCATGCTGCTCCCCAGCTGGAAAACAAGTTCTTATGTGGGTGCCAGCATTGTGACAG
CAGTTGGCTTCTCCAAGGGCCTCTGGATGGAATGTGCCACACACAGCACAGGCATCACCCAG
TGTGACATCTATAGCACCTTCTGGGCCTGCCCCGCTGACATCCAGGCTGCCCAGGCCATGAT
GGTGACATCCAGTGCAATCTCCTCCCTGGCCTGCATTATCTCTGTGGTGGGCATGAGATGCA
CAGTCTTCTGCCAGGAATCCCGAGCCAAAGACAGAGTGGCGGTAGCAGGTGGAGTCTTTTTTC
ATCCTTGGAGGCCTCCTGGGATTCAATCCTGTTGCCTGGAATCTTCATGGGATCCTACGGGA
CTTCTACTCACCACTGGTGCCTGACAGCATGAAATTTGAGATTGGAGAGGCTCTTTACTTGG
GCATTATTTCTTCCCTGTTCTCCCTGATAGCTGGAATCATCCTCTGCTTTTCTGCTCATCC
CAGAGAAATCGCTCCAACCTACTACGATGCCTACCAAGCCCCAACCTCTTGCCACAAGGAGCTC
TCCAAGGCCTGGTCAACCTCCCAAAGTCAAGAGTGAGTTCAATTCCTACAGCCTGACAGGGT
ATGTGTGAAGAACCAGGGGCCAGAGCTGGGGGGTGGCTGGGTCTGTGAAAAACAGTGGACAG
CACCCCGAGGGCCACAGGTGAGGGACACTACCACTGGATCGTGTCAGAAGGTGCTGCTGAGG
ATAGACTGACTTTGGCCATTGGATTGAGCAAAGGCAGAAATGGGGGCTAGTGTAACAGCATG
CAGGTTGAATTGCCAAGGATGCTCGCCATGCCAGCCTTTCTGTTTTCTCACCTTGCTGCTC
CCCTGCCCTAAGTCCCCAACCTCAACTTGAAACCCCATTCCTTAAGCCAGGACTCAGAGG
ATCCCTTTGCCCTCTGGTTTACCTGGGACTCCATCCCCAAACCCACTAATCACATCCCCTG
ACTGACCCTCTGTGATCAAAGACCCTCTCTCTGGCTGAGGTTGGCTCTTAGCTCATTGCTGG
GGATGGGAAGGAGAAGCAGTGGCTTTTGTGGGCATTGCTCTAACCTACTTCTCAAGCTTCCC
TCCAAAGAAACTGATTGGCCCTGGAACCTCCATCCCCTCTTGTTATGACTCCACAGTGTCC
AGACTAATTTGTGCATGAACTGAAATAAAACCATCCTACGGTATCCAGGGAACAGAAAGCAG
GATGCAGGATGGGAGGACAGGAAGGCAGCCTGGGACATTTAAAAAATA

FIGURE 78

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64886
><subunit 1 of 1, 230 aa, 1 stop
><MW: 24549, pI: 8.56, NX(S/T): 1
MASLGLQLVGYILGLLGTLVAMLLPSWKTSSYVGASIVTAVGFSKGLWMECATHSTGIT
QCDIYSTLLGLPADIQAAQAMMVTSSAISSLACIISVVGMRCTVFCQESRAKDRVAVAGGVF
FILGLLGFIPVAWNLHGILRDFYSPLVPDSMKFEIGEALYLGIISSLFSLIAGIILCFSCS
SQNRNSNYDAYQAQPLATRSSPRPGQPPKVKSEFNSYSLTGYV

Important features of the protein:**Signal peptide:**

amino acids 1-24

Transmembrane domains:

amino acids 82-102, 117-140, 163-182

N-glycosylation site.

amino acids 190-193

PMP-22 / EMP / MP20 family proteins.

amino acids 46-59

FIGURE 79

GCACTGCTGCTGTCCCATCAGCTGCTCTGAAGCTCCATGGTGCCCAGAATCTTCGCTCCTGC
TTATGTGTCAGTCTGTCTCCTCCTCTTGTGTCCAAGGGAAGTCATCGCTCCCGCTGGCTCAG
AACCATGGCTGTGCCAGCCGGCACCCAGGTGTGGAGACAAGATCTACAACCCCTTGGAGCAG
TGCTGTTACAATGACGCCATCGTGTCCCTGAGCGAGACCCGCCAATGTGGTCCCCCCTGCAC
CTTCTGGCCCTGCTTTGAGCTCTGCTGTCTTGATTCCTTTGGCCTCACAAACGATTTTGTG
TGAAGCTGAAGGTTTCAGGGTGTGAATTCCTAGTGCCACTCATCTCCCATCTCCAGTAAATGT
GAAAGCAGAAGACGTTTTCCCTTGAGAAGACATAGAAAGAAAATCAACTTTCCTAAGGCATC
TCAGAAACATAGGCTAAGGTAATATGTGTACCAGTAGAGAAGCCTGAGGAATTTACAAAATG
ATGCAGCTCCAAGCCATTGTATGGCCCATGTGGGAGACTGATGGGACATGGAGAATGACAGT
AGATTATCAGGAAATAAATAAAGTGGTTTTTCCAATGTACACACCTGTAAAA

FIGURE 80

MVPRIFAPAYVSVCLLLCPREVIAPAGSEPWLCQPAPRCGDKIYNPLEQCCYNDIVSLSE
TRQCGPPCTFWPCFELCCLDSFGLTNDVFVVKLVQGVNSQCHSSPISSKCESRRRFP

Signal peptide:
amino acids 1-25

80/270

FIGURE 81

CTCCACTGCAACCACCCAGAGCCATGGCTCCCCGAGGCTGCATCGTAGCTGTCTTTGCCATT
TTCTGCATCTCCAGGCTCCTCTGCTCACACGGAGCCCCAGTGGCCCCCATGACTCCTTACCT
GATGCTGTGCCAGCCACACAAGAGATGTGGGGACAAGTTCTACGACCCCCCTGCAGCACTGTT
GCTATGATGATGCCGTCGTGCCCTTGGCCAGGACCCAGACGTGTGGAAACTGCACCTTCAGA
GTCTGCTTTGAGCAGTGCTGCCCCCTGGACCTTCATGGTGAAGCTGATAAACCAGAACTGCCA
CTCAGCCCCGGACCTCGGATGACAGGCTTTGTGCGAGTGTGAGCTTAATGGAACATCAGGGGAA
CGATGACTCCTGGATTCTCCTTCCTGGGTGGGCCTGGAGAAAGAGGCTGGTGTACCTGAGA
TCTGGGATGCTGAGTGGCTGTTTGGGGGCCAGAGAAACACACACTCAACTGCCCACTTCATT
CTGTGACCTGTCTGAGGCCACCCCTGCAGCTGCCCTGAGGAGGCCACAGGTCCCCCTTCTAG
AATTCTGGACAGCATGAGATGCGTGTGCTGATGGGGGCCAGGGACTCTGAACCCTCCTGAT
GACCCCTATGGCCAACATCAACCCGGCACCACCCCAAGGCTGGCTGGGGAACCCCTTCACCCT
TCTGTGAGATTTTCCATCATCTCAAGTTCTCTTCTATCCAGGAGCAAAGCACAGGATCATAA
TAAATTTATGTACTTTATAAATGAAAA

FIGURE 82

MAPRGCIVAVFAIFCISRLLC SHGAPVAPMTPYLMLCQPHKRCGDKFYDPLQHCCYDDAVVP
LARTQTCGNCTFRVCFEQCCPWTFMVKLINQNCD SARTSDDR LCRSVS

Signal peptide:
amino acids 1-24

82/270

FIGURE 83

GGGGGCGGGTGCCTGGAGCACGGCGCTGGGGCCGCCCCGCAGCGCTCACTCGCTCGCACTCAG
TCGCGGGAGGCTTCCCCGCGCCGGCCGCTCCCGCCCGCTCCCCGGCACCAGAAGTTCCTCT
GCGCGTCCGACGGCGACATGGGCGTCCCCACGGCCCTGGAGGCCGGCAGCTGGCGCTGGGGA
TCCCTGCTCTTCGCTCTCTTCTGGCTGCGTCCCTAGGTCCGGTGGCAGCCTTCAAGGTCGC
CACGCCGTATTCCCTGTATGTCTGTCCCGAGGGGCAGAACGTCAACCCTCACCTGCAGGCTCT
TGGGCCCTGTGGACAAAGGGCACGATGTGACCTTCTACAAGACGTGGTACCGCAGCTCGAGG
GGCGAGGTGCAGACCTGCTCAGAGCGCCGGCCCATCCGCAACCTCACGTTCCAGGACCTTCA
CCTGCACCATGGAGGCCACCAGGCTGCCAACACCAGCCACGACCTGGCTCAGCGCCACGGGC
TGGAGTCGGCCTCCGACCACCATGGCAACTTCTCCATCACCATGCGCAACCTGACCTGCTG
GATAGCGGCCTCTACTGCTGCCTGGTGGTGGAGATCAGGCACCACCACTCGGAGCACAGGGT
CCATGGTGGCATGGAGCTGCAGGTGCAGACAGGCAAAGATGCACCATCCAACCTGTGTGGTGT
ACCCATCCTCCTCCAGGATAGTGAAAAATCACGGCTGCAGCCCTGGCTACGGGTGCCCTGC
ATCGTAGGAATCCTCTGCCTCCCCCTCATCCTGCTCCTGGTCTACAAGCAAAGGCAGGCAGC
CTCCAACCGCCGTGCCAGGAGCTGGTGGGATGGACAGCAACATTCAAGGGATTGAAAACC
CCGGCTTTGAAGCCTCACCACCTGCCCAGGGGATACCCGAGGCCAAAGTCAGGCACCCCTG
TCCTATGTGGCCAGCGGCAGCCTTCTGAGTCTGGGCGGCATCTGCTTTCGGAGCCCAGCAC
CCCCCTGTCTCTCCAGGCCCGGAGACGTCTTCTTCCCATCCCTGGACCCTGTCCCTGACT
CTCCAAACTTTGAGGTCATCTAGCCCAGCTGGGGGACAGTGGGCTGTTGTGGCTGGGTCTGG
GGCAGGTGCATTTGAGCCAGGGCTGGCTCTGTGAGTGGCCTCCTTGGCCTCGGCCCTGGTTC
CCTCCCTCCTGCTCTGGGCTCAGATACTGTGACATCCCAGAAGCCAGCCCCCTCAACCCCTC
TGGATGCTACATGGGGATGCTGGACGGCTCAGCCCCTGTTCCAAGGATTTTGGGGTGCTGAG
ATTCTCCCCCTAGAGACCTGAAATTACACAGCTACAGATGCCAAATGACTTACATCTTAAGAA
GTCTCAGAACGTCCAGCCCTTCAGCAGCTCTCGTTCTGAGACATGAGCCTTGGGATGTGGCA
GCATCAGTGGGACAAGATGGACACTGGGCCACCCTCCCAGGCACCAGACACAGGGCACGGTG
GAGAGACTTCTCCCCCGTGGCCGCCTTGGCTCCCCCGTTTGGCCGAGGCTGCTCTTCTGTC
AGACTTCCTCTTTGTACCACAGTGGCTCTGGGGCCAGGCCTGCCTGCCCCTGGCCATCGCC
ACCTTCCCCAGCTGCCCTCCTACCAGCAGTTTCTCTGAAGATCTGTCAACAGGTTAAGTCAAT
CTGGGGCTTCCACTGCCTGCATTCCAGTCCCAGAGCTTGGTGGTCCCGAAACGGGAAGTAC
ATATTGGGGCATGGTGGCCTCCGTGAGCAAATGGTGTCTTGGGCAATCTGAGGCCAGGACAG
ATGTTGCCCCACCCACTGGAGATGGTGTGAGGGAGGTGGGTGGGGCCTTCTGGGAAGGTGA
GTGGAGAGGGGCACCTGCCCCCGCCCTCCCCATCCCCCTACTCCCACTGCTCAGCGCGGGCC
ATTGCAAGGGTGCCACACAATGTCTTGTCCACCCTGGGACACTTCTGAGTATGAAGCGGGAT
GCTATTAAAAACTACATGGGGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAGA

FIGURE 84

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64897

><subunit 1 of 1, 311 aa, 1 stop

><MW: 33908, pI: 6.87, NX(S/T): 6

MGVPTALEAGSWRWGSLLFALFLAASLGPVAAFVKVATPYSLYVCEPQNVTLTCRLLGPVDK
GHDVTFYKTYWRSSRGEVQTCSERRPIRNLTFQDLHLHHGGHQAANTSHDLAQRHGLESASD
HHGNFSITMRNLTLDDSGLYCCLVVEIRHHHSEHRVHGAMELQVQTGKDAPSNVCVYPSSSQ
DSENITAAALATGACIVGILCLPLILLVYKQQAASNRRAQELVRMDSNIQGIENPGFEAS
PPAQGIPEAKVRHPLSYVAQRQPSESGRHLLSEPSTPLSPPGPGDVFFPSLDPVPDSPNFEVI

Signal peptide:

amino acids 1-28

Transmembrane domain:

amino acids 190-216

FIGURE 85

CCCACGCGTCCGCGCCTCTCCCTTCTGCTGGACCTTCCTTCGTCTCTCCATCTCTCCCTCCT
TTCCCCGCGTTCTCTTTCCACCTTTCTCTTCTTCCACCTTAGACCTCCCTTCCTGCCCTCC
TTCTCTGCCCCACCGCTGCTTCCTGGCCCTTCTCCGACCCCGCTCTAGCAGCAGACCTCCTGG
GGTCTGTGGGTTGATCTGTGGCCCCCTGTGCCTCCGTGTCCTTTTCGTCTCCCTTCCTCCCGA
CTCCGCTCCCGGACCAGCGGCCTGACCCTGGGGAAAGGATGGTTCCCGAGGTGAGGGTCCTC
TCCTCCTTGCTGGGACTCGCGCTGCTCTGGTTCCCCCTGGACTCCCACGCTCGAGCCCGCCC
AGACATGTTCTGCCTTTTCCATGGGAAGAGATACTCCCCGGCGAGAGCTGGCACCCCTACT
TGGAGCCACAAGGCCTGATGTACTGCCTGCGCTGTACCTGCTCAGAGGGCGCCCATGTGAGT
TGTTACCGCCTCCACTGTCCGCCTGTCCACTGCCCCCAGCCTGTGACGGAGCCACAGCAATG
CTGTCCCAAGTGTGTGGAACCTCACACTCCCTCTGGACTCCGGGCCCCACCAAAGTCCTGCC
AGCACAACGGGACCATGTACCAACACGGAGAGATCTTCAGTGCCCATGAGCTGTTCCCTCC
CGCCTGCCCAACCAGTGTGTCTCTGCAGCTGCACAGAGGGCCAGATCTACTGCGGCCTCAC
AACCTGCCCCGAACCAGGCTGCCCAGCACCCCTCCCACTGCCAGACTCCTGTGCCAAGCCT
GCAAAGATGAGGCAAGTGAGCAATCGGATGAAGAGGACAGTGTGCAGTCGCTCCATGGGGTG
AGACATCCTCAGGATCCATGTTCCAGTGATGCTGGGAGAAAGAGAGGCCCGGGCACCCACAGC
CCCCACTGGCCTCAGCGCCCCCTCTGAGCTTCATCCCTCGCCACTTCAGACCCAAGGGAGCAG
GCAGCACAACCTGTCAAGATCGTCCTGAAGGAGAAACATAAGAAAGCCTGTGTGCATGGCGGG
AAGACGTACTCCACGGGGAGGTGTGGCACCCGGCCTTCCGTGCCTTCGGCCCCCTTGCCCTG
CATCCTATGCACCTGTGAGGATGGCCGCCAGGACTGCCAGCGTGTGACCTGTCCCACCGAGT
ACCCCTGCCGTCACCCCGAGAAAGTGGCTGGGAAGTGCTGCAAGATTTGCCCAGAGGACAAA
GCAGACCCTGGCCACAGTGAGATCAGTTCTACCAGGTGTCCAAGGCACCGGGCCGGGTCTCT
CGTCCACACATCGGTATCCCCAAGCCCAGACAACCTGCGTCGCTTTGCCCTGGAACACGAGG
CCTCGGACTTGGTGGAGATCTACCTCTGGAAGCTGGTAAAAGATGAGGAACTGAGGCTCAG
AGAGGTGAAGTACCTGGCCCAAGGCCACACAGCCAGAATCTTCCACTTGACTCAGATCAAGA
AAGTCAGGAAGCAAGACTTCAGAAAGAGGCACAGCACTTCCGACTGCTCGCTGGCCCCCAC
GAAGGTCACTGGAACGTCTTCCTAGCCCAGACCCTGGAGCTGAAGGTCACGGCCAGTCCAGA
CAAAGTGACCAAGACATAACAAAGACCTAAACAGTTGCAGATATGAGCTGTATAATTGTTGTT
ATTATATATTAATAAATAAGAAGTTGCATTACCCTCAAAAAAAAAAAAAAAAAAAAAA

FIGURE 86

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64902

><subunit 1 of 1, 451 aa, 1 stop

><MW: 49675, pI: 7.15, NX(S/T): 1

MVPEVRVLSSLLGLALLWFPLDSHARARPDMFCLFHGKRYSPGESWHYPYLEPQGLMYCLRCT
CSEGAHVSCYRLHCPPVHCPQPVTEPQQCCPKCVEPHTPSGLRAPPKSCQHNGTMYQHGEIF
SAHELFPSRLPNQCVLCSCTEGQIYCGLTTCPEPGCPAPLPLPDSCCQACKDEASEQSDEED
SVQSLHGVRHPQDPCSSDAGRKRGPGTAPPTGLSAPLSFIPRHFRPKGAGSTTVKIVLKEKH
KKACVHGGKTYSHGEVWHPAFRAFGPLPCILCTCEDGRQDCQRVTCPTTEYPCRHPKRVAGKC
CKICPEDKADPGHSEISSTRCPKAPGRVLVHTSVSPSPDNLRRFALEHEASDLVEIYLWKLV
KDEETEAQRGEVPGPRPHSQNLPLDSDQESQEARLPERGTALPTARWPPRSLERLPSDPDG
AEGHGQSRQSDQDITKT

Signal peptide:

amino acids 1-25

86/270

FIGURE 87

CTAGCCTGCGCCAAGGGGTAGTGAGACCGCGCGGCAACAGCTTGCGGCTGCGGGGAGCTCCC
GTGGGCGCTCCGCTGGCTGTGCAGGCGGCCATGGATTCCCTTGCGGAAAATGCTGATCTCAGT
CGCAATGCTGGGCGCAGGGGCTGGCGTGGGCTACGCGCTCCTCGTTATCGTGACCCCGGGAG
AGCGGCGGAAGCAGGAAATGCTAAAGGAGATGCCACTGCAGGACCCAAGGAGCAGGGAGGAG
GCGGCCAGGACCCAGCAGCTATTGCTGGCCACTCTGCAGGAGGCAGCGACCACGCAGGAGAA
CGTGGCCTGGAGGAAGAACTGGATGGTTGGCGGCGAAGGCGGCGCCAGCGGGAGGTCACCGT
GAGACCGGACTTGCCCTCCGTGGGCGCCGGACCTTGGCTTGGGCGCAGGAATCCGAGGCAGCC
TTTCTCCTTCGTGGGCCCAGCGGAGAGTCCGGACCGAGATACCATGCCAGGACTCTCCGGGG
TCCTGTGAGCTGCCGTGCGGTGAGCACGTTTCCCCCAAACCCTGGACTGACTGCTTTAAGGT
CCGCAAGGCGGGCCAGGGCCGAGACGCGAGTCGGATGTGGTGAAGTGAAGAACAATAAAA
TCATGTTCTCCAA
AAAAAAAAAAAA

FIGURE 88

MDSLRLKMLISVAMLGAGAGVGYALLVIVTPGERRKQEMLKEMPLQDPRSREEAARTQQLLLA
TLQEAATTQENVAWRKNWMVGGEGGASGRSP

Signal peptide:
amino acids 1-18

FIGURE 89

CAGGAGAGAAGGCACCGCCCCACCCCGCCTCCAAAGCTAACCCCTCGGGCTTGAGGGGAAGA
GGCTGACTGTACGTTCCCTTCTACTCTGGCACCCTCTCCAGGCTGCCATGGGGCCCAGCACC
CCTCTCCTCATCTTGTTCCCTTTTGTTCATGGTGGGACCCCTCCAAGGACAGCAGCACCACCT
TGTGGAGTACATGGAACCGGACTAGCTGCTTTAGAGGAACGGCTGGCCAGTGCCAGGACC
AGAGTAGTCGGCATGCTGCTGAGCTGCGGGACTTCAAGAACAAGATGCTGCCACTGCTGGAG
GTGGCAGAGAAGGAGCGGGAGGCACCTCAGAACTGAGGCCGACACCATCTCCGGGAGAGTGGA
TCGTCTGGAGCGGGAGGTAGACTATCTGGAGACCCAGAACCAGCTCTGCCCTGTGTAGAGT
TTGATGAGAAGGTGACTGGAGGCCCTGGGACCAAAGGCAAGGGAAGAAGGAATGAGAAGTAC
GATATGGTGACAGACTGTGGCTACACAATCTCTCAAGTGAGATCAATGAAGATTCTGAAGCG
ATTTGGTGGCCCAGCTGGTCTATGGACCAAGGATCCACTGGGGCAAACAGAGAAGATCTACG
TGTTAGATGGGACACAGAATGACACAGCCTTTGTCTTCCCAAGGCTGCGTGACTTCACCCTT
GCCATGGCTGCCCCGAAAGCTTCCCGAGTCCGGGTGCCCTTCCCCTGGGTAGGCACAGGGCA
GCTGGTATATGGTGGCTTTCTTTATTTTGTCTGGAGGCCTCCTGGAAGACCTGGTGGAGGTG
GTGAGATGGAGAACACTTTGCAGCTAATCAAATTCACCTGGCAAACCGAACAGTGGTGGAC
AGCTCAGTATTTCCAGCAGAGGGGCTGATCCCCCCTACGGCTTGACAGCAGACACCTACAT
CGACCTGGTAGCTGATGAGGAAGGTCTTTGGGCTGTCTATGCCACCCGGGAGGATGACAGGC
ACTTGTGTCTGGCCAAGTTAGATCCACAGACACTGGACACAGAGCAGCAGTGGGACACACCA
TGTCACAGAGAGAATGCTGAGGCTGCCTTTGTTCATCTGTGGGACCCTCTATGTCTCTATAA
CACCCGTCTGCCAGTCGGGCCCCGATCCAGTGCTCCTTTGATGCCAGCGGCACCCTGACCC
CTGAACGGGCAGCACTCCCTTATTTTCCCCGAGATATGGTGCCCATGCCAGCCTCCGCTAT
AACCCCGAGAACGCCAGCTCTATGCCTGGGATGATGGCTACCAGATTGTCTATAAGCTGGA
GATGAGGAAGAAAGAGGAGGAGGTTTGAGAGGCTAGCCTTGTTTTTTGCATCTTTCTCACTC
CCATACATTTATATTATATCCCCACTAAATTTCTTGTTCCCTCATCTTCAAATGTGGGCCAG
TTGTGGCTCAAATCCTCTATATTTTGTAGCCAATGGCAATCAAATCTTTTCTAGCTCCTTTGTT
TCATACGGAACCTCAGATCCTGAGTAATCCTTTTAGAGCCCGAAGAGTCAAACCCCTCAATG
TTCCCTCCTGCTCTCCTGCCCCATGTCAACAAATTTTCTAGGCTAAGGATGCCCCAGACCCAGG
GCTCTAACCTTGATGCGGGCAGGCCAGGGAGCAGGCAGCAGTGTCTTCCCCTCAGAGTG
ACTTGGGGAGGGAGAAATAGGAGGAGACGTCCAGCTCTGTCCTCTCTTCTCACTCCTCCCT
TCAGTGTCTGAGGAACAGGACTTTCTCCACATTGTTTTGTATTGCAACATTTTGCATTAAA
AGGAAAATCCACAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 90

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64905

<subunit 1 of 1, 406 aa, 1 stop

<MW: 46038, pI: 6.50, NX(S/T): 2

MGPSTPLLLILFLLSWGPLQGQQHHLVEYMERRLAALAEERLAQCQDQSSRHAAELRDFKNKM
LPLLEVAEKEREALRTEADTISGRVDRLEREVDYLETONPALPCVEFDEKVTGGPGTKGKGR
RNEKYDMVTDGCGYTISQVRSMKILKRFGGPAGLWTKDPLGQTEKIYVLDGTQNDTAFVFPRL
RDFTLAMAARKASRVVPFPWVGTLVYGGFLYFARRPPGRPGGGGEMENTLQLIKFHLAN
RTVVDSSVFPAEGLIPPYGLTADTYIDLVADEEGLWAVYATREDDRHLCCLAKLDPQTLDEQ
QWDTPCPRENAEAAAFVICGTLVYVYNTRPASRARIQCSFDASGTLTPERAALPYFPRRYGAH
ASLRYNPRERQLYAWDDGYQIVYKLEMRKKEEEV

Important features:

Signal peptide:

amino acids 1-21

N-glycosylation sites.

amino acids 177-180, 248-251

90/270

FIGURE 91

GACAGCTGTGTCTCGATGGAGTAGACTCTCAGAACAGCGCAGTTTGCCTCCGCTCACGCAG
AGCCTCTCCGTGGCTTCCGCACCTTGAGCATTAGGCCAGTTCTCCTCTTCTCTAATCCAT
CCGTACCTCTCCTGTCATCCGTTTCCATGCCGTGAGGTCCATTACAGAACACATCCATGG
CTCTCATGCTCAGTTTGGTTCTGAGTCTCCTCAAGCTGGGATCAGGGCAGTGGCAGGTGTTT
GGGCCAGACAAGCCTGTCCAGGCCCTTGGTGGGGGAGGACGCAGCATTCTCCTGTTTCCTGTC
TCCTAAGACCAATGCAGAGGCCATGGAAGTGCGGTTCTTCAGGGGCCAGTTCTCTAGCGTGG
TCCACCTCTACAGGGACGGGAAGGACCAGCCATTATGCAGATGCCACAGTATCAAGGCAGG
ACAAACTGGTGAAGGATTCTATTGCGGAGGGGCGCATCTCTCTGAGGCTGGAAAACATTAC
TGTGTTGGATGCTGGCCTCTATGGGTGCAGGATTAGTTCCCAGTCTTACTACCAGAAGGCCA
TCTGGGAGCTACAGGTGTCTGCTCAGTCTCGGGCTGGTTCCCCCGGGCCACAGCGAAGTG
GAAAGGTCCACAAGGACAGGATTTGTCCACAGACTCCAGGACAAACAGAGACATGCATGGCC
TGTTTGATGTGGAGATCTCTCTGACCGTCCAAGAGAACGCCGGGAGCATATCCTGTTCCATG
CGGCATGCTCATCTGAGCCGAGAGGTGGAATCCAGGGTACAGATAGGAGATACCTTTTTTCGA
GCCTATATCGTGGCACCTGGCTACCAAAGTACTGGGAATACTCTGCTGTGGCCTATTTTTTG
GCATTGTTGGACTGAAGATTTTCTTCTCAAATTCAGTGGAAAATCCAGGCCGAACTGGAC
TGGAGAAGAAAGCACGGACAGGCAGAATTGAGAGACGCCCGAAACACGCAGTGGAGGTGAC
TCTGGATCCAGAGACGGCTCACCCGAAGCTCTGCGTTTCTGATCTGAAAACGTAAACCCATA
GAAAAGCTCCCCAGGAGGTGCCTCACTCTGAGAAGAGATTTACAAGGAAGAGTGTGGTGGCT
TCTCAGAGTTTCCAAGCAGGGAAACATTACTGGGAGGTGGACGGAGGACACAATAAAAGGTG
GCGCGTGGGAGTGTGCCGGGATGATGTGGACAGGAGGAAGGAGTACGTGACTTTGTCTCCCG
ATCATGGGTACTGGGTCTCAGACTGAATGGAGAACATTTGTATTTACATTAAATCCCCGT
TTTATCAGCGTCTTCCCCAGGACCCACCTACAAAAATAGGGGTCTTCCTGGACTATGAGTG
TGGGACCATCTCCTTCTTCAACATAAATGACCAGTCCCTTATTTATACCCTGACATGTGGT
TTGAAGGCTTATTGAGGCCCTACATTGAGTATCCGTCTTATAATGAGCAAAATGGAATCCC
ATAGTCATCTGCCAGTCACCCAGGAATCAGAGAAAGAGGCCTCTTGGCAAAGGGCCTCTGC
AATCCCAGAGACAAGCAACAGTGAGTCCTCCTCACAGGCAACCACGCCCTTCTCCCCAGGG
GTGAAATGTAGGATGAATCACATCCCACATTCTTCTTTAGGGATATTAAGGTCTCTCTCCA
GATCCAAAGTCCCGCAGCAGCCGGCCAAGGTGGCTTCAGATGAAGGGGGACTGGCCTGTCC
ACATGGGAGTCAGGTGTCTGGCTGCCCTGAGCTGGGAGGGAAGAAGGCTGACATTACATTT
AGTTTGCTCTCACTCCATCTGGCTAAGTGATCTTGAAATACCACCTCTCAGGTGAAGAACCG
TCAGGAATTTCCATCTCACAGGCTGTGGTGTAGATTAAGTAGACAAGGAATGTGAATAATGC
TTAGATCTTATTGATGACAGAGTGATCCTAATGGTTTGTTCATTATATTACACTTTCAGTA
AAAAAA

FIGURE 92

MALMLSLVLSLLKLGSGQWQVFGPDKPVQALVGEDAAFSCFLSPKTNAEAMEVRFFRGQFSS
VHLYRDGKDQPFMQMPQYQGR TKLVKDSIAEGRISLRLENITVLDAGLYGCRIS SQSYQK
AIWELQVSALGSVPLISITGYVDRDIQLLCQSSGWFP RP TAKWKGPQGQDLSTD SRTNRDMH
GLFDVEISLTVQENAGSISCSMRHAHLSREVESRVQIGDTFFEPISWHLATKVLGILCCGLF
FGIVGLKIFFSKFQWKIQAELDWRRKHGQAE LRDARKHAVEVTLD PETAH PKLCVSDLKTVT
HRKAPQEVPHSEKRFRTRKSVVASQSFQAGKHYWEVDGGHNKRWRVGVCRDDVDRRKEYVTLS
PDHGYWVLRLNGEHL YFTLNPRFISVFPRTPPTKIGVFLDYECGTISFFNINDQSLIYTLTC
RFEGLLRPYIEYPSYNEQNGTPIVICPVTQESEKEASWQRASAI PETSNSSESSQATTPFLP
RGEM

Signal peptide:

amino acids 1-17

Transmembrane domain:

amino acids 239-255

FIGURE 93

GCGATGGTGC GCCCGGTGGCGGTGGCGGGCGGCGGTTGCGGAGGCTTCCTTGGTTCGGATTGCA
ACGAGGAGAAGATGACTGACCAACCGACTGGCTGAATGAATGAATGGCGGAGCCGAGCGCGC
CATGAGGAGCCTGCCGAGCCTGGGCGGCCTCGCCCTGTTGTGCTGCGCCGCCGCCGCCGCCG
CCGTGCGCTCAGCCGCCCTCGGCGGGGAATGTCACCGGTGGCGGCGGGGCCGCGGGGCAGGTG
GACGCGTCGCCGGGCCCCGGGTGCGGGGCGAGCCCAGCCACCCCTTCCCTAGGGCGACGGC
TCCCACGGCCCCAGGCCCCGAGGACCGGGCCCCCGCGCGCCACCGTCCACCGACCCCTGGCTG
CGACTTCTCCAGCCCAGTCCCCGGAGACCACCCCTCTTTGGGCGACTGCTGGACCCTCTTCC
ACCACCTTTCAGGCGCCGCTCGGCCCTCGCCGACCACCCCTCCGGCGGGCGGAACGCACTTC
GACCACCTCTCAGGCGCCGACCAGACCCGCGCCGACCACCCCTTTCGACGACCACTGGCCCCG
CGCCGACCACCCCTGTAGCGACCACCGTACCGGCGCCACGACTCCCCGGACCCCGACCCCC
GATCTCCCCAGCAGCAGCAACAGCAGCGTCCCTCCCCACCCACCTGCCACCGAGGCCCCCTC
TTCGCTCCTCCAGAGTATGTATGTAACCTGCTCTGTGGTTGGAAGCCTGAATGTGAATCGCT
GCAACCAGACCACAGGGCAGTGTGAGTGTGCGCCAGGTTATCAGGGGCTTACTGTGAAACC
TGCAAAGAGGGCTTTTACCTAAATTACACTTCTGGGCTCTGTGAGCCATGTGACTGTAGTCC
ACATGGAGCTCTCAGCATAACCGTGCAACAGGTAAGCAACAGAGGGTGGAAGTGAAGTTTATT
TTATTTTAGCAAGGGAAAAAAGGCTGCTACTCTCAAGGACCATACTGGTTTAAACAAAG
GAGGATGAGGGTCATAGATTTACAAAATATTTTATATACTTTTATTCTCTTACTTTATATGT
TATATTTAATGTGAGGATTTAAAAACATCTAATTTACTGATTTAGTTCTTCAAAAGCACTAG
AGTCGCCAATTTTTCTCTGGGATAATTTCTGTAAATTTATGGGAAAAAATTATTGAAGAAT
AAATCTGCTTTCTGGAAGGGCTTTAGGCATGAAACCTGCTAGGAGGTTTAGAAATGTTCTT
ATGTTTATTAATATAACCATTTGAGTTTGAGGAAATTTGTTGTTTGGTTTATTTTCTCTCTA
ATCAAAATTTCTACATTTGTTTCTTTGGACATCTAAAGCTTAACCTGGGGGTACCTAATTTA
TTTAACCTAGTGGTAAGTAGACTGGTTTTACTCTATTTACCAGTACATTTTGGAGACCAAAAG
TAGATTAAGCAGGAATTATCTTTAACTATTATGTTATTTGGAGGTAATTTAATCTAGTGGA
ATAATGTACTGTTATCTAAGCATTGCTTGTACTGCACTGAAAGTAATTATCTTTGACCT
TATGTGAGGCACTTGGCTTTTTGTGGACCCCAAGTCAAAAACTGAAGAGACAGTATTAAT
AATGAAAAAATAATGACAGGTTATACTCAGTGTAACCTGGGTATAACCAAGATCTGCTGC
CACTTACGAGCTGTGTTCTTGGGCAAGTAATTTCTTTCACTGAGCTTGTCTTCTCAAG
GTTGTTGTGAAGATTAAATGAGTTGATATATATAAAATGCCTAGCACATGTCACTCAATAAA
TTCTGGTTTGTTTTAAATTTCAAAGGAATATTATGGACTGAAATGAGAGAACATGTTTAAAG
ACTTTTAGCTCCTTGACAAAGAAGTGCTTTATACTTTAGCACTAAATATTTTAAATGCTTTA
TAAATGATATTATACTGTTATGGAATATTGTATCATATTGTAGTTTATTAAAAATGTAGAAG
AGGCTGGGCGCGGTGGCTCACGCCTGTAATCCTAGCACTTTGGGAGGCCAAGCGGGTGGAT
CACTTGAGGCCAGGAGTTCTAGATGAGCCTGGCCAGCACAGTGAAACCCGTCTCTACTAAA
AATACAAACAAATTAGCTGGGCGTGGTGGCACACACCTGTAGTCCCAGCTACTCGGGAGGCT
GAGGCAGGAGAATCGGTTGAACCCGGGAGGTGGAGGTTGCAGTGAGCTGAGATCGCGCCACT
GCACTCCAGCCTGGTGAGAGAGGGAGACTCTGTCTTAAAAA

FIGURE 94

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64952

><subunit 1 of 1, 258 aa, 1 stop

><MW: 25716, pI: 8.13, NX(S/T): 5

M R S L P S L G G L A L L C C A A A A A V A S A A S A G N V T G G G G A A G Q V D A S P G P G L R G E P S H P F P R A T A
P T A Q A P R T G P P R A T V H R P L A A T S P A Q S P E T T P L W A T A G P S S T T F Q A P L G P S P T T P P A A E R T S
T T S Q A P T R P A P T T L S T T T G P A P T T P V A T T V P A P T T P R T P T P D L P S S S N S S V L P T P P A T E A P S
S P P P E Y V C N C S V V G S L N V N R C N Q T T G Q C E C R P G Y Q G L H C E T C K E G F Y L N Y T S G L C Q P C D C S P
H G A L S I P C N R

Important features of the protein:

Signal peptide:

amino acids 1-25

N-glycosylation sites.

amino acids 30-33, 172-175, 195-198, 208-211, 235-238

EGF-like domain cysteine pattern signature.

amino acids 214-226.

FIGURE 95

TGCGGCGCAGTGTAGACCTGGGAGGATGGGCGGCCTGCTGCTGGCTGCTTTTCTGGCTTTGG
TCTCGGTGCCCAGGGCCCAGGCCGTGTGGTTGGGAAGACTGGACCCCTGAGCAGCTTCTTGGG
CCCTGGTACGTGCTTGCAGTGGCCTCCCGGGAAAAGGGCTTTGCCATGGAGAAGGACATGAA
GAACGTCGTGGGGGTGGTGGTGACCCCTACTCCAGAAAACAACCTGCGGACGCTGTCTCTC
AGCACGGGCTGGGAGGGTGTGACCAGAGTGTTCATGGACCTGATAAAGCGAAACTCCGGATGG
GTGTTTGAGAATCCCTCAATAGGCGTGCTGGAGCTCTGGGTGCTGGCCACCAACTTCAGAGA
CTATGCCATCATCTTCACTCAGCTGGAGTTCGGGGACGAGCCCTTCAACACCGTGGAGCTGT
ACAGTCTGACGGAGACAGCCAGCCAGGAGGCCATGGGGCTCTTCACCAAGTGGAGCAGGAGC
CTGGGCTTCCTGTACAGTTAGCAGGCCCAGCTGCAGAAGGACCTCACCTGTGCTCACAAAGAT
CCTTCTGTGAGTGCTGCGTCCCCAGTAGGGATGGCGCCACAGGGTCTGTGACCTCGGCCA
GTGTCCACCCACCTCGCTCAGCGGCTCCCGGGGCCAGCACCAGCTCAGAATAAAGCGATTCC
CACAGCA

FIGURE 96

MGGLLLAFLALVSVPRQAVWLGRDLPEQLLGPWYVLAVASREKGFAMEKDMKNVVGVVVT
LTPENNLRTLSSQHGLGGCDQSVMDLIKRN SGWVFENPSIGVLELWVLATNFRDYAIIFTQL
EFGDEPFNTVELYSLTETASQEAMGLFTKWSRSLGFLSQ

Signal peptide:

amino acids 1-20

FIGURE 97

AACAGACGTTCCCTCGCGGCCCTGGCACCTCTAACCCAGACATGCTGCTGCTGCTGCTGCC
CCTGCTCTGGGGGAGGGAGAGGGCGGAAGGACAGACAAGTAACTGCTGACGATGCAGAGTT
CCGTGACGGTGACAGGAAGGCCTGTGTGTCCATGTGCCCTGCTCCTTCTCCTACCCCTCGCAT
GGCTGGATTACCTTGGCCCAGTAGTTCATGGCTACTGGTTCGCGGAAGGGGCCAATACAGA
CCAGGATGCTCCAGTGGCCACAAACAACCCAGCTCGGGCAGTGTGGGAGGAGACTCGGGACC
GATTCCACCTCCTTGGGGACCCACATACCAAGAATTGCACCCTGAGCATCAGAGATGCCAGA
AGAAGTGATGCGGGGAGATACTTCTTTCGTATGGAGAAAGGAAGTATAAAATGGAATTATAA
ACATCACCGGCTCTCTGTGAATGTGACAGCCTTGACCCACAGGCCCAACATCCTCATCCCAG
GCACCCTGGAGTCCGGCTGCCCCAGAATCTGACCTGCTCTGTGCCCTGGGCCTGTGAGCAG
GGGACACCCCTATGATCTCCTGGATAGGGACCTCCGTGTCCCCCTGGACCCCTCCACCAC
CCGCTCCTCGGTGCTCACCCCTCATCCACAGCCCCAGGACCATGGCACCAGCCTCACCTGTC
AGGTGACCTTCCCTGGGGCCAGCGTGACCACGAACAAGACCGTCCATCTCAACGTGTCCTAC
CCGCCTCAGAACTTGACCATGACTGTCTTCCAAGGAGACGGCACAGTATCCACAGTCTTGGG
AAATGGCTCATCTCTGTCACTCCCAGAGGGCCAGTCTCTGCGCCTGGTCTGTGCAGTTGATG
CAGTTGACAGCAATCCCCCTGCCAGGCTGAGCCTGAGCTGGAGAGGCCTGACCCTGTGCCCC
TCACAGCCCTCAAACCCGGGGGTGCTGGAGCTGCCTTGGGTGCACCTGAGGGATGCAGCTGA
ATTACCTGCAGAGCTCAGAACCTCTCGGCTCTCAGCAGGTCTACCTGAACGTCTCCCTGC
AGAGCAAAGCCACATCAGGAGTGACTCAGGGGGTGGTCGGGGGAGCTGGAGCCACAGCCCTG
GTCTTCCTGTCTTCTGCGTCATCTTCGTTGTAGTGAGGTCTGCAGGAAGAAATCGGCAAG
GCCAGCAGCGGGCGTGGGAGATACGGGCATAGAGGATGCAAACGCTGTGAGGGGTTGAGCCT
CTCAGGGGCCCCCTGACTGAACCTTGGGCAGAAGACAGTCCCCCAGACCAGCCTCCCCAGCT
TCTGCCCCGCTCCTCAGTGGGGGAAGGAGAGCTCCAGTATGCATCCCTCAGCTTCCAGATGGT
GAAGCCTTGGGACTCGCGGGGACAGGAGGCCACTGACACCGAGTACTCGGAGATCAAGATCC
ACAGATGAGAACTGCAGAGACTCACCTGATTGAGGGATCACAGCCCCCTCCAGGCAAGGGA
GAAGTCAGAGGCTGATTCTTGTAGAATTAACAGCCCTCAACGTGATGAGCTATGATAACACT
ATGAATTATGTGCAGAGTGAAAAGCACACAGGCTTTAGAGTCAAAGTATCTCAAACCTGAAT
CCACACTGTGCCCTCCCTTTTATTTTTTTAACTAAAAGACAGACAAATTCCTA

FIGURE 98

MLLLLLPLLLWGRERAEGQTSKLLTMQSSVTVQEGLCVHVPCSF SYPSHGWIYPGPVVHGYWF
REGANTDQDAPVATNNPARAVWEETRDRFHLLGDPHTKNCTLSIRDARRSDAGRYFFRMEKG
SIKWNYPKHRLSVNVTALTHRPNILIPGTLESGCPQNLTCVWPWACEQGTPPMISWIGTSVS
PLDPSTTRSSVLTLPQPQDHGTS LTCQVTFPGASVTTNKTVHLNVSYPPQNLMTVFQGDG
TVSTVLGNGSSLSLPEGQSLRLVCAVDAVDSNPPARLSLSWRGLTLCPSQPSNPGVLELPWV
HLRDAAEFTCRAQNPLGSQQVYLNVS LQSKATSGVTQGVVGGAGATALVFLSFCVIFVVVRS
CRKKSARPAAGVGDTGIEDANAVRG SASQGPLEPWAEDSPPDQPPASARSSVGE GELQYA
SLSFQMVKPWDSRGQEATDTEYSEIKIHR

Signal peptide:

amino acids 1-15

Transmembrane domain:

amino acids 351-370

FIGURE 99

GACGCCCAGTGACCTGCCGAGGTCGGCAGCACAGAGCTCTGGAGATGAAGACCCTGTTTCCTG
GGTGTACGCTCGGCCTGGCCGCTGCCCTGTCCTTCACCCTGGAGGAGGAGGATATCACAGG
GACCTGGTACGTGAAGGCCATGGTGGTCGATAAGGACTTTCGGGAGGACAGGAGGCCAGGA
AGGTGTCCCCAGTGAAGGTGACAGCCCTGGGCGGTGGGAAGTTGGAAGCCACGTTACCTTC
ATGAGGGAGGATCGGTGCATCCAGAAGAAAATCCTGATGCGGAAGACGGAGGAGCCTGGCAA
ATACAGCGCCTATGGGGGCAGGAAGCTCATGTACCTGCAGGAGCTGCCAGGAGGGACCACT
ACATCTTTTACTGCAAAGACCAGCACCATGGGGGCCTGCTCCACATGGGAAAGCTTGTGGGT
AGGAATTCTGATACCAACCGGGAGGCCCTGGAAGAATTTAAGAAATTGGTGCAGCGCAAGGG
ACTCTCGGAGGAGGACATTTTCACGCCCCCTGCAGACGGGAAGCTGCGTTCCCGAACACTTAGG
CAGCCCCCGGGTCTGCACCTCCAGAGCCCACCCTACCACCAGACACAGAGCCCGGACCACCT
GGACCTACCCTCCAGCCATGACCCTTCCCTGCTCCACCCACCTGACTCCAAATAAAGTCCT
TTTCCCCCAA

FIGURE 100

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA65404

<subunit 1 of 1, 170 aa, 1 stop

<MW: 19457, pI: 9.10, NX(S/T): 0

MKTLFLGVTLGLAAALSFTLEEDITGTWYVKAMVVDKDFPEDRRPRKVSPVKVTALGGGKL

EATFTFMREDRCIQKKILMRKTEEPGKYSAYGGRKLMYLQELPRRDHYIFYCKDQHHGGLLH

MGKLVGRNSDTNREALEEFKKLVQRKGLSEEDIFTPLQTGSCVPEH

Important features:

Signal peptide:

amino acids 1-17

100/270

FIGURE 101

GTTCCGCAGATGCAGAGGTTGAGGTGGCTGCGGGACTGGAAGTCATCGGGCAGAGGTCTCAC
AGCAGCCAAGGAACCTGGGGCCCGCTCCTCCCCCTCCAGGCCATGAGGATTCTGCAGTTAA
TCCTGCTTGCTCTGGCAACAGGGCTTGTTAGGGGGAGAGACCAGGATCATCAAGGGGTTTCGAG
TGCAAGCCTCACTCCCAGCCCTGGCAGGCAGCCCTGTTTCGAGAAGACGCGGCTACTCTGTGG
GGCGACGCTCATCGCCCCAGATGGCTCCTGACAGCAGCCCACTGCCTCAAGCCCCGCTACA
TAGTTCACCTGGGGCAGCACAACTCCAGAAGGAGGAGGGCTGTGAGCAGACCCGGACAGCC
ACTGAGTCCTTCCCCACCCCGGCTTCAACAACAGCCTCCCCAACAAAGACCACCGCAATGA
CATCATGCTGGTGAAGATGGCATCGCCAGTCTCCATCACCTGGGCTGTGCGACCCCTCACCC
TCTCCTCACGCTGTGTCACTGCTGGCACCAGCTGCCTCATTTCCGGCTGGGGCAGCACGTCC
AGCCCCCAGTTACGCCTGCCTCACACCTTGCGATGCGCCAACATCACCATCATTGAGCACCA
GAAGTGTGAGAACGCCTACCCCGGCAACATCACAGACACCATGGTGTGTGCCAGCGTGCAGG
AAGGGGGCAAGGACTCCTGCCAGGGTGACTCCGGGGGCCCTCTGGTCTGTAACCAGTCTCTT
CAAGGCATTATCTCCTGGGGCCAGGATCCGTGTGCGATCACCCGAAAGCCTGGTGTCTACAC
GAAAGTCTGCAAATATGTGGACTGGATCCAGGAGACGATGAAGAACAATTAGACTGGACCCA
CCCACCACAGCCCATCACCCCTCCATTTCCACTTGGTGTGTTGGTTCCCTGTTCACTCTGTTAAT
AAGAAACCCTAAGCCAAGACCCTCTACGAACATTCTTTGGGCCTCCTGGACTACAGGAGATG
CTGTCACTTAATAATCAACCTGGGGTTTCGAAATCAGTGAGACCTGGATTCAAATTCTGCCTT
GAAATATTGTGACTCTGGGAATGACAACACCTGGTTTGTCTCTGTTGTATCCCCAGCCCCA
AAGACAGCTCCTGGCCATATATCAAGGTTTCAATAAATATTGCTAAATGAAAAAAAAAAAAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 102

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA65405

<subunit 1 of 1, 250 aa, 1 stop

<MW: 27466, pI: 8.87, NX(S/T): 4

MRILQLILLALATGLVGGETRIIKGFECKPHSQPWQAALFEKTRLLCGATLIAPRWLLTAAH
CLKPRYIVHLGQHNLQKEEGCEQTRTATESFPHPGFNNSLPNKDHRNDIMLVKMASPV SITW
AVRPLTLSSRCV TAGTSC LISGWGSTSSPQLRLPHTLR CANITIEHQKCENAYPGNITDTM
VCASVQEGGKDSCQGD SGGPLVCNQSLQGIISWGQDPCAITRKPGVYTKVCKYVDWIQETMKNN

Important features:

Signal peptide:

amino acids 1-18

Serine proteases, trypsin family, histidine active site.

amino acids 58-63

N-glycosylation sites.

amino acids 99-102, 165-168, 181-184, 210-213

Glycosaminoglycan attachment site.

amino acids 145-148

Kringle domain proteins.

amino acids 197-209, 47-64

Serine proteases, trypsin family, histidine protein

amino acids 199-209, 47-63, 220-243

Apple domain proteins

amino acids 222-249, 189-222

102/270

FIGURE 103

GAGCAGTGTCTGCTGGAGCCGATGCCAAAAACCATGCATTCTTATTCAGATTCATTGTTT
TCTTTTATCTGTGGGGCCTTTTTACTGCTCAGAGACAAAAGAAAGAGGAGAGCACCGAAGAA
GTGAAAATAGAAGTTTTGCATCGTCCAGAAAACCTGCTCTAAGACAAGCAAGAAGGGAGACCT
ACTAAATGCCCATTATGACGGCTACCTGGCTAAAGACGGCTCGAAATTCTACTGCAGCCGGA
CACAAAATGAAGGCCACCCCAAATGGTTTGTCTTGGTGTGGGCAAGTCATAAAAGGCCTA
GACATTGCTATGACAGATATGTGCCCTGGAGAAAAGCGAAAAGTAGTTATACCCCCTTCATT
TGCATACGGAAAGGAAGGCTATGCAGAAGGCAAGATTCCACCGGATGCTACATTGATTTTG
AGATTGAACTTTATGCTGTGACCAAAGGACCACGGAGCATTGAGACATTTAAACAAATAGAC
ATGGACAATGACAGGCAGCTCTCTAAAGCCGAGATAAACCTCTACTTGCAAAGGGAATTTGA
AAAAGATGAGAAGCCACGTGACAAGTCATATCAGGATGCAGTTTTAGAAGATATTTTAAAGA
AGAATGACCATGATGGTGATGGCTTCATTTCTCCAAGGAATACAATGTATACCAACACGAT
GAACTATAGCATATTTGTATTTCTACTTTTTTTTTTTTAGCTATTTACTGTACTTTATGTATA
AAACAAAGTCACTTTTCTCCAAGTTGTATTTGCTATTTTTCCCCTATGAGAAGATATTTGA
TCTCCCCAATACATTGATTTTGGTATAATAAATGTGAGGCTGTTTTGCAAACCTTAAAAAAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 104

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA65406

<subunit 1 of 1, 222 aa, 1 stop

<MW: 25794, pI: 6.24, NX(S/T): 1

MPKTMHFLFRFIVFFYLLWGLFTAQRQKKEESTEEVKIEVLHRPENCSKTSKKGDLLNAHYDG
YLAKDGSKFYCSRTQNEGHPKWFVLGVGQVIKGLDIAMTDMCPGEKRKVVIPPSFAYGKEGY
AEGKIPPDATLIFEIELYAVTKGPRSIETFKQIDMDNDRQLSKAEINLYLQREFEKDEKPRD
KSYQDAVLEDIFKKNDHGDGDFISPKEYNVYQHDEL

Important features:

Endoplasmic reticulum targeting sequence.

amino acids 219-222

N-glycosylation site.

amino acids 45-48

FKBP-type peptidyl-prolyl cis-trans isomerase

amino acids 87-223, 129-142

EF-hand calcium-binding domain proteins

amino acids 202-214, 195-214

104/270

FIGURE 105

CAGAAATGCAGGGACCATTGCTTCTTCCAGGCCTCTGCTTTCTGCTGAGCCTCTTTGGAGCT
GTGACTCAGAAAACCAAACTTCCTGTGCTAAGTGCCCCCAAATGCTTCCTGTGTCAATAA
CACTCACTGCACCTGCAACCATGGATATACTTCTGGATCTGGGCAGAACTATTACATTCC
CCTTGGAGACATGTAACGCCAGGCATGGTGGCTCGCGCCTGTAACCCAGTTCTTTGGGAAG
CCAAGGCAGGTGGATCACCTGAGGTCAGGAGTTTGAGACCAGCCTGGCCAACATAGTGAAAC
CCCGTGTCTACTAAAAATACAAAAATCAGCCGGGCGTGTTGGTGCATGCCTGCAATCCCAGT
TACTCGGGAGGCTGAGGCAGGAGAATCGCTTGAATCAGGAGGCAGAAGTTGCAGTGAACCC
AGATCCTGCCATTGCACTCCAGCATGGATGACAGAGCAAGACTCCGTCTCAAAAAGAAAAGA
TAGTTTCTTGTTTCATTTGCGGACTGCCCTCTCAGTGTTTCCTGGGATCCCCTCCCAAATAA
AGTACTTATATTCTC

FIGURE 106

MQGPLLLLPGLCFLLSLFGAVTQKTKTSCAKCPPNASCVNNTHCTCNHGYTSGSGQKLFTFPL
ETCNARHGG SRL

Signal peptide:
amino acids 1-18

106/270

FIGURE 107

CAAGCAGGTCATCCCCTTGGTGACCTTCAAAGAGAAGCAGAGAGGGCAGAGGTGGGGGGGCAC
AGGGAAAGGGTGACCTCTGAGATTCCCCTTTTCCCCCAGACTTTGGAAGTGACCCACCATGG
GGCTCAGCATCTTTTGTCTCCTGTGTGTTCTTGGGCTCAGCCAGGCAGCCACACCGAAGATT
TTCAATGGCACTGAGTGTGGGCGTAACTCACAGCCGTGGCAGGTGGGGCTGTTTGAGGGGCAC
CAGCCTGCGCTGCGGGGGTGTCTTATTGACCACAGGTGGGTCTCACAGCGGCTCACTGCA
GCGGCAGCAGGTACTGGGTGCGCCTGGGGGAACACAGCCTCAGCCAGCTCGACTGGACCGAG
CAGATCCGGCACAGCGGCTTCTCTGTGACCCATCCCGGCTACCTGGGAGCCTCGACGAGCCA
CGAGCACGACCTCCGGCTGCTGCGGCTGCGCCTGCCCCTCCGCGTAACCAGCAGCGTTCAAC
CCCTGCCCCCTGCCCAATGACTGTGCAACCGCTGGCACCGAGTGCCACGTCTCAGGCTGGGGC
ATCACCAACCACCCACGGAACCCATTCCCGGATCTGCTCCAGTGCCTCAACCTCTCCATCGT
CTCCCATGCCACCTGCCATGGTGTGTATCCCGGGAGAATCACGAGCAACATGGTGTGTGCAG
GCGGCGTCCCGGGGCAGGATGCCTGCCAGGGTGATTCTGGGGGCCCCCTGGTGTGTGGGGGA
GTCCTTCAAGGTCTGGTGTCTGGGGGTCTGTGGGGCCCTGTGGACAAGATGGCATCCCTGG
AGTCTACACCTATATTTGCAAGTATGTGGACTGGATCCGGATGATCATGAGGAACAACTGAC
CTGTTTCTCTCCACCTCCACCCCCACCCCTTAACCTTGGGTACCCCTCTGGCCCTCAGAGCACC
AATATCTCCTCCATCACTTCCCCTAGCTCCACTCTTGTTGGCCTGGGAACCTTCTTGGAACCTT
TAACTCCTGCCAGCCCTTCTAAGACCCACGAGCGGGGTGAGAGAAGTGTGCAATAGTCTGGA
ATAAATATAAATGAAGGAGGGGCAAAAAAAAAAAAAA

FIGURE 108

MGLSIFLLLCVLGLSQAATPKIFNGTECGRNSQPWQVGLFEGTSLRCGGVLIDHRWVLTAAH
CSGSRYWVRLGEHSLSQLDWTEQIRHSGFSVTHPGYLGASTSHEHDLRLRLRLPVRVTSSV
QPLPLPNDCATAGTECHVSGWGITNHPRNPFDPDLLQCLNLSIVSHATCHGVYPGRITSNMVC
AGGVPGQDACQGDSGGPLVCGGVLQGLVSWGSVGPCGQDGIPGVYTYICKYVDWIRMIMRNN

Signal peptide:

amino acids 1-17

FIGURE 109

GCGGCCACACGCAGCTAGCCGGAGCCCGGACCAGGCGCCTGTGCCTCCTCCTCGTCCCTCGC
CGCGTCCGCGAAGCCTGGAGCCGGCGGGAGCCCCGCGCTCGCCATGTCGGGCGAGCTCAGCA
ACAGGTTCCAAGGAGGGAAGGCGTTCGGCTTGCTCAAAGCCCGGCAGGAGAGGAGGCTGGCC
GAGATCAACCGGGAGTTTCTGTGTGACAGAGAAGTACAGTGATGAAGAGAACCTTCCAGAAAA
GCTCACAGCCTTCAAAGAGAAGTACATGGAGTTTGACCTGAACAATGAAGGCGAGATTGACC
TGATGTCTTTAAAGAGGATGATGGAGAAGCTTGGTGTCCCAAGACCCACCTGGAGATGAAG
AAGATGATCTCAGAGGTGACAGGAGGGGTGAGTGACACTATATCCTACCGAGACTTTGTGAA
CATGATGCTGGGGAAACGGTCGGCTGTCCTCAAGTTAGTCATGATGTTTGAAGGAAAAGCCA
ACGAGAGCAGCCCCAAGCCAGTTGGCCCCCCTCCAGAGAGAGACATTGCTAGCCTGCCCTTGA
GGACCCCGCCTGGACTCCCCAGCCTTCCCACCCCATACCTCCCTCCCGATCTTGCTGCCCTT
CTTGACACACTGTGATCTCTCTCTCTCATTTGTTTGGTCATTGAGGGTTTGTGTTGTTT
TCATCAATGTCTTTGTAAAGCACAAATTATCTGCCTTAAAGGGGCTCTGGGTGGGGAATCC
TGAGCCTTGGGTCCCCCTCCCTCTCTTCTTCCCTCCTTCCCCGCTCCCTGTGCAGAAGGGCTG
ATATCAAACCAAAAAGTAGAGGGGGCAGGGCCAGGGCAGGGAGGCTTCCAGCCTGTGTTCCC
CTCACTTGGAGGAACCAGCACTCTCCATCCTTTCAGAAAGTCTCCAAGCCAAGTTCAGGCTC
ACTGACCTGGCTCTGACGAGGACCCCAGGCCACTCTGAGAAGACCTTGGAGTAGGGACAAGG
CTGCAGGGCCTCTTTCGGGTTTCCTTGGACAGTGCCATGGTTCAGTGCTCTGGTGTCACCC
AGGACACAGCCACTCGGGGCCCCGCTGCCCCAGCTGATCCCCACTCATTCCACACCTCTTCT
CATCCTCAGTGATGTGAAGGTGGGAAGGAAAGGAGCTTGGCATTGGGAGCCCTTCAAGAAGG
TACCAGAAGGAACCCTCCAGTCCTGCTCTCTGGCCACACCTGTGCAGGCAGCTGAGAGGCAG
CGTGCAGCCCTACTGTCCCTTACTGGGGCAGCAGAGGGCTTCGGAGGCAGAAGTGAGGCCTG
GGGTTTGGGGGGAAGGTCAGCTCAGTGCTGTTCCACCTTTTAGGGAGGATACTGAGGGGAC
CAGGATGGGAGAATGAGGAGTAAAATGCTCACGGCAAAGTCAGCAGCACTGGTAAGCCAAGA
CTGAGAAATACAAGGTTGCTTGTCTGACCCCAATCTGCTTGAAAAAAAAAAAAAAAAAAAAA

FIGURE 110

MSGELSNRFQGGKAFGLLKARQERRLAEGINREFLCDQKYSDEENLPEKLTAFKEKYMEFDLN
NEGEIDLMSLKRMMEKLGVPKTHLEMKKMISEVTGGVSDTISYRDFVNMMLGKRSAVLKLV
MFEGKANESSPKPVGPPPERDIASLP

FIGURE 111A

CGCGCTCCCCGCGCGCCTCCTCGGGCTCCACGCGTCTTGCCCCGCAGAGGCAGCCTCCTCCA
GGAGCGGGGCCCTGCACACCATGGGCCCCCGGGTGGGCAGGGGTGGGCGCCGCCGTGCGCGCC
CGCCTGGCGCTGGCCTTGGCGCTGGCGAGCGTCTGAGTGGGCCTCCAGCCGTGCGCTGCCC
CACCAAGTGTACCTGCTCCGCTGCCAGCGTGGACTGCCACGGGCTGGGCCTCCGCGCGGTTC
CTCGGGGCATCCCCCGCAACGCTGAGCGCCTTGACCTGGACAGAAATAATATCACCAGGATC
ACCAAGATGGACTTCGCTGGGCTCAAGAACCTCCGAGTCTTGCACTCTGGAAGACAACCAGGT
CAGCGTCATCGAGAGAGGCGCCTTCCAGGACCTGAAGCAGCTAGAGCGACTGCGCCTGAACA
AGAATAAGCTGCAAGTCCTTCCAGAATTGCTTTTCCAGAGCACGCCGAAGCTCACCAGACTA
GATTTGAGTGAAAACCAGATCCAGGGGATCCCGAGGAAGGCGTTCGCGGCATCACCGATGT
GAAGAACCTGCAACTGGACAACAACCACATCAGCTGCATTGAAGATGGAGCCTTCCGAGCGC
TGCGCGATTTGGAGATCCTTACCCTCAACAACAACAACATCAGTCGCATCCTGGTCACCAGC
TTCAACCACATGCCGAAGATCCGAACCTCTGCGCCTCCACTCCAACCACCTCTACTGCGACTG
CCACCTGGCCTGGCTCTCGGATTGGCTGCGACAGCGACGGACAGTTGGCCAGTTCACACTCT
GCATGGCTCCTGTGCATTTGAGGGGCTTCAACGTGGCGGATGTGCAGAAGAAGGAGTACGTG
TGCCCAGCCCCCACTCGGAGCCCCCATCCTGCAATGCCAACTCCATCTCCTGCCTTCCGCC
CTGCACGTGCAGCAATAACATCGTGGACTGTGCGAGGAAAGGGCTTGATGGAGATTCTTGCCA
ACTTGCCGGAGGGCATCGTCGAAATACGCCTAGAACAGAACTCCATCAAAGCCATCCCTGCA
GGAGCCTTCACCCAGTACAAGAACTGAAGCGAATAGACATCAGCAAGAATCAGATATCGGA
TATTGCTCCAGATGCCTTCCAGGGCCTGAAATCACTCACATCGCTGGTCTGTATGGGAACA
AGATCACCGAGATTGCCAAGGGACTGTTTGATGGGCTGGTGTCCCTACAGCTGCTCCTCCTC
AATGCCAACAAGATCAACTGCCTGCGGGTGAACACGTTTCAGGACCTGCAGAACCTCAACTT
GCTCTCCCTGTATGACAACAAGCTGCAGACCATCAGCAAGGGGCTCTTCGCCCCCTCTGCAGT
CCATCCAGACACTCCACTTAGCCCCAAAACCCATTTGTGTGCGACTGCCACTTGAAGTGGCTG
GCCGACTACCTCCAGGACAACCCCATCGAGACAAGCGGGGCCCGCTGCAGCAGCCCGCGCCG
ACTCGCCAACAAGCGCATCAGCCAGATCAAGAGCAAGAAGTTCCGCTGCTCAGGCTCCGAGG
ATTACCGCAGCAGGTTTCCAGCAGCGAGTGCTTCATGGACCTCGTGTGCCCCGAGAAGTGTGCG
TGTGAGGGCACGATTGTGGACTGCTCCAACCAGAAGCTGGTCCGCATCCCAAGCCACCTCCC
TGAATATGTCACCGACCTGCGACTGAATGACAATGAGGTATCTGTTCTGGAGGCCACTGGCA
TCTTCAAGAAGTTGCCCAACCTGCGGAAAATAAATCTGAGTAACAATAAGATCAAGGAGGTG
CGAGAGGGAGCTTTTCGATGGAGCAGCCAGCGTGCAGGAGCTGATGCTGACAGGGAACCAGCT
GGAGACCGTGCACGGGCGCGTGTTCGCTGGCCTCAGTGGCCTCAAACCTTGATGCTGAGGA
GTAACCTTGATCAGCTGTGTGAGTAATGACACCTTTGCCGGCCTGAGTTCGGTGAGACTGCTG
TCCCTCTATGACAATCGGATCACCACCATCACCCCTGGGGCCTTCACCACGCTTGTCTCCCT
GTCCACCATAAACCTCCTGTCCAACCCCTTCAACTGCAACTGCCACCTGGCCTGGCTCGGCA
AGTGGTTGAGGAAGAGGCGGATCGTCAGTGGGAACCCTAGGTGCCAGAAGCCATTTTTCCTC
AAGGAGATTCCCATCCAGGATGTGGCCATCCAGGACTTCACCTGTGATGGCAACGAGGAGAG
TAGCTGCCAGCTGAGCCCGCGCTGCCCGGAGCAGTGCACCTGTATGGAGACAGTGGTGGCAT
GCAGCAACAAGGGGCTCCGCGCCCTCCCAGAGGCATGCCCAAGGATGTGACCGAGCTGTAC
CTGGAAGGAAACCACCTAACAGCCGTGCCAGAGAGCTGTCCGCCCTCCGACACCTGACGCT
TATTGACCTGAGCAACAACAGCATCAGCATGCTGACCAATTACACCTTCAGTAACATGTCTC
ACCTCTCCACTCTGATCCTGAGCTACAACCGGCTGAGGTGCATCCCCGTCCACGCCTTCAAC
GGGCTGCGGTCCCTGCGAGTGCTAACCCCTCCATGGCAATGACATTTCCAGCGTTCTTGAAGG
CTCCTTCAACGACCTCACATCTCTTCCCATCTGGCGCTGGGAACCAACCCACTCCACTGTG
ACTGCAGTCTTCGGTGGCTGTGCGAGTGGGTGAAGGCGGGGTACAAGGAGCCTGGCATCGCC
CGCTGCAGTAGCCCTGAGCCCATGGCTGACAGGCTCCTGCTCACCACCCCAACCCACCGCTT
CCAGTGCAAAGGGCCAGTGGACATCAACATTGTGGCCAAATGCAATGCCTGCCTCTCCAGCC
CGTGCAAGAATAACGGGACATGCACCCAGGACCCTGTGGAGCTGTACCGCTGTGCCTGCCCC

FIGURE 111B

TACAGCTACAAGGGCAAGGACTGCACTGTGCCCATCAACACCTGCATCCAGAACCCCTGTCA
GCATGGAGGCACCTGCCACCTGAGTGACAGCCACAAGGATGGGTTTCACTGCTCCTGCCCTC
TGGGCTTTGAGGGGAGCGGTGTGAGATCAACCCAGATGACTGTGAGGACAACGACTGCGAA
AACAATGCCACCTGCGTGGACGGGATCAACAACCTACGTGTGTATCTGTCCGCTAAGTACAC
AGGTGAGCTATGCGACGAGGTGATTGACCACTGTGTGCCTGAGCTGAACCTCTGTCAGCATG
AGGCCAAGTGCATCCCCCTGGACAAAGGATTGAGCTGCGAGTGTGTCCCTGGCTACAGCGGG
AAGCTCTGTGAGACAGACAATGATGACTGTGTGGCCCAAGTGCCGCCACGGGGCCCAGTG
CGTGGACACAATCAATGGCTACACATGCACCTGCCCCCAGGGCTTCAGTGGACCCTTCTGTG
AACACCCCCCACCCTATGGTCCCTACTGCAGACCAGCCCATGCGACCAGTACGAGTGCCAGAAC
GGGGCCCAGTGCATCGTGGTGCAGCAGGAGCCACCTGCCGCTGCCACCAGGCTTCGCCGG
CCCCAGATGCGAGAAGCTCATCACTGTCAACTTCGTGGGCAAAGACTCCTACGTGGAAGTGG
CCTCCGCCAAGGTCCGACCCAGGCCAACATCTCCCTGCAGGTGGCCACTGACAAGGACAAC
GGCATCCTTCTCTACAAAGGAGACAATGACCCCTGGCACTGGAGCTGTACCAGGGCCACGT
GCGGCTGGTCTATGACAGCCTGAGTTCCTCCCAACCACAGTGTACAGTGTGGAGACAGTGA
ATGATGGGCAGTTTACAGTGTGGAGCTGGTGACGCTAAACCAGACCCTGAACCTAGTAGTG
GACAAAGGAACTCCAAAGAGCCTGGGGAAGCTCCAGAAGCAGCCAGCAGTGGGCATCAACAG
CCCCCTCTACCTTGGAGGCATCCCCACCTCCACCGGCCTCTCCGCCTTGCGCCAGGGCACGG
ACCGGCCTCTAGGCGGCTTCCACGGATGCATCCATGAGGTGCGCATCAACAACGAGCTGCAG
GACTTCAAGGCCCTCCCACCACAGTCCCTGGGGGTGTACCAGGCTGCAAGTCTGCACCGT
GTGCAAGCACGGCCTGTGCCGCTCCGTGGAGAAGGACAGCGTGGTGTGCGAGTGCCGCCAG
GCTGGACCGGCCCCACTCTGCGACCAGGAGGCCCGGGACCCCTGCCTCGGCCACAGATGCCAC
CATGGAAAATGTGTGGCAACTGGGACCTCATAATGTGCAAGTGTGCCGAGGGCTATGGAGG
GGACTTGTGTGACAACAAGAATGACTCTGCCAATGCCTGCTCAGCCTTCAAGTGTACCATG
GGCAGTGCCACATCTCAGACCAAGGGGAGCCCTACTGCCTGTGCCAGCCCGGCTTTAGCGGC
GAGCACTGCCAACAAGAGAATCCGTGCCTGGGACAAGTAGTCCGAGAGGTGATCCGCCGCCA
GAAAGGTTATGCATCATGTGCCACAGCCTCCAAGGTGCCCATCATGGAATGTCGTGGGGGCT
GTGGGCCCCAGTGCTGCCAGCCCAACCGCAGCAAGCGGCGGAAATACGTCTTCCAGTGCACG
GACGGCTCCTCGTTTGTAGAAGAGGTGGAGAGACACTTAGAGTGCGGCTGCCTCGCGTGTTC
CTAAGCCCCCTGCCCGCCTGCCTGCCACCTCTCGGACTCCAGCTTGATGGAGTTGGGACAGCC
ATGTGGGACCCCTGGTGATTGAGCATGAAGGAAATGAAGCTGGAGAGGAAGGTAAAGAAGA
AGAGAATATTAAGTATATTGTAAAATAAACAAAAAATAGAACTAAAAAAAAAAAAAAAAAA
AAAAAA

FIGURE 112

MAPGWAGVGAAVRARLALALALASVLSGPPAVACPTKCTCSAASVDCHGLGLRAVPRGI PRN
AERLDLDRNNITRITKMDFAGLKNLRVLHLEDNQVSVIERGAFQDLKQLERLRLNKNKLQVL
PELLFQSTPKLTRLDLSENQIQGIPRKAFRGITDVKNLQLDNNHISCIEDGAFRALRDLEIL
TLNNNNISRI LVT SFNHMPKIRTLRLHSNHLYCDCHLAWLSDWLRQRRTVGQFTLCMAPVHL
RGFNVADVQKKEYVCPAPHSEPPSCNANSISCPSPCTCSNNIVDCRGKGLMEIPANLPEGIV
EIRLEQNSIKAIPAGAFTQYKKLKRIDISKNQISDIAPDAFQGLKSLTSLVLYGNKITEIAK
GLFDGLVSLQLLLLNANKINCLRVNTFQDLQNLNLLSLYDNKLQTI SKGLFAPLQSIQTLHL
AQNP FVCDCHLKW LADYLQDNPIETSGARCSSPRRLANKRISQIKSKKFRCSGSEDYRSRFS
SECFMDLVCPEKCRCEGTIVDCSNQKLVRI PSHLPEYVTDLRLNDNEVSVLEATGIFKKLPN
LRKINLSNNKIKEVREGAFDGAASVQELMLTGNQLETVHGRVFRGLSGLKTLMLRSNLISCV
SNDTFAGLSSVRLLSLYDNRI TTITPGAFTTLVSLSTINLLSNPFNCNCHLAWLGKWLKRKR
IVSGNPRCQKPFFLKEIPIQDVAIQDFTCDGNEESSCQLSPRCPEQCTCMETVVRC SNKGLR
ALPRGMPKDVTELYLEG NHLTAVPRELSALRH LTLIDLSNNSISMLTNYTFSNM SHLSTLIL
SYNRLRCIPVHAFNGLRSLRVLT LHGNDISSVPEGSFNDLTSLSHLALGTNPLHCD CSLRWL
SEWVKAGYKEPGIARCSSPEPMADRLLLTTPTHR FQCKGPVDINIVAKCNACLSSPCKNNGT
CTQDPVELYRCACPYSYKGDCTVPINTCIQNPCQHGGTCHLSDSHKDGFSCSCPLGFEGQR
CEINPDDCEDNDCENNATCVDGINNYVCICPPNYTGELCDEVIDHCVPELNLCQHEAKCIPL
DKGFSCECVPGYSGKLCETDNDDCVAHKCRHGAQCVDTINGYTCTCPQGFSGPFCEHPPPMV
LLQTSPCDQYECQNGAQCIVVQQEPTCRCPPGFAGPRCEKLI TVNFVGKDSYVELASAKVRP
QANISLQVATDKDNGILLYKGDNDPLALELYQGHVRLVYDSLSSPPTTVYSVETVNDGQFHS
VELVTLNQTLNLVVDKGT PKSLGKLQKQPAVGINSPLYLGGIPTSTGLSALRQGTDRPLGGF
HGCIEVRINNELQDFKALPPQSLGVSPGCKSCTVCKHGLCRSVEKDSVCECRPGWTGPLC
DQEARDPCLGHRCHHGKCVATGTSYMCKCAEGYGGDLCDNKND SANACSAFKCHHGQCHISD
QGEPYCLCQPGFSGEHCQQENPCLGQVVREVIRRQKGYASCATASKVPIMECRGGCGPQCCQ
PTRSKRRKYVFQCTDGSSFVEEVERHLECGCLACS

Signal peptide:

amino acids 1-27

FIGURE 113

GGATGCAGGACGCTCCCCTGAGCTGCCTGTCACCGACTAGGTGGAGCAGTGTTTCTTCCGCA
GACTCAACTGAGAAGTCAGCCTCTGGGGCAGGCACCAGGAATCTGCCTTTTCAGTTCTGTCT
CCGGCAGGCTTTGAGGATGAAGGCTGCGGGCATTCTGACCCTCATTGGCTGCCTGGTCACAG
GCGCCGAGTCCAAAATCTACACTCGTTGCAAACCTGGCAAAAATATTCTCGAGGGCTGGCCTG
GACAATTACTGGGGCTTCAGCCTTGGAACCTGGATCTGCATGGCATATTATGAGAGCGGCTA
CAACACCACAGCCCCGACGGTCCTGGATGACGGCAGCATCGACTATGGCATCTTCCAGATCA
ACAGCTTCGCGTGGTGCAGACGCGGAAAGCTGAAGGAGAACAACTGCCATGTGCGCTGC
TCAGCCTTGATCACTGATGACCTCACAGATGCAATTATCTGTGCCAGGAAAATTGTTAAAGA
GACACAAGGAATGAACTATTGGCAAGGCTGGAAGAAACATTGTGAGGGCAGAGACCTGTCCG
AGTGGAAAAAAGGCTGTGAGGTTTCCTTAAACTGGAACCTGGACCCAGGATGCTTTGCAGCAAC
GCCCTAGGATTTGCAGTGAATGTCCAAATGCCTGTGTCATCTTGTCCCGTTTCCTCCCAATA
TTCCTTCTCAAACCTGGAGAGGGGAAAATTAAGCTATACTTTTAAGAAAATAAATATTTCCAT
TTAAATGTC

FIGURE 114

MKAAGILTLIGCLVTGAESKIYTRCKLAKIFSRAGLDNYWGFS LGNWICMAYYESGYNTTAP
TVLDDGSIDYGIFQINSFAWCRRGKCLKENNHCHVACSALITDDLTDALICARKIVKETQGMN
YWQGWKKHCEGRDLSEWKKGCEVS

Signal peptide:

amino acids 1-19

FIGURE 115

CAGGCCATTTGCATCCCACTGTCTTGTGTTTCGGAGCCAGGCCACACCGTCCTCAGCAGTGT
CATGTGTTAAAAACGCCAAGCTGAATATATCATGCCCCCTATTAAAACTTGTACATGGCTCCC
CATTGGTTTTTTGGAGAAAAGTTCAAGCTTTTTTACCTTGGTGTCTGCCTGTATCCCAGTGTTC
AGGCTGGCTAGACGGCGGAAGAAGATCCTATTTTTACTGTCACTTCCCAGATCTGCTTCTCAC
CAAGAGAGATTCTTTTCTTAAACGACTATACAGGGCCCCAATTGACTGGATAGAGGAATACA
CCACAGGCATGGCAGACTGCATCTTAGTCAACAGCCAGTTCACAGCTGCTGTTTTTAAGGAA
ACATTCAAGTCCCTGTCTCACATAGACCCTGATGTCTCTATCCATCTCTAAATGTCACCAG
CTTTGACTCAGTTGTTTCTGAAAAGCTGGATGACCTAGTCCCCAAGGGGAAAAAATTCCTGC
TGCTCTCCATCAACAGATACGAAAGGAAGAAAAATCTGACTTTGGCACTGGAAGCCCTAGTA
CAGCTGCGTGGAAGATTGACATCCCAAGATTGGGAGAGGGTTCATCTGATCGTGGCAGGTGG
TTATGACGAGAGAGTCTTGGAGAATGTGGAACATTATCAGGAATTGAAGAAAATGGTCCAAC
AGTCCGACCTTGGCCAGTATGTGACCTTCTTGAGGTCTTCTCAGACAAACAGAAAATCTCC
CTCCTCCACAGCTGCACGTGTGTGCTTTACACACCAAGCAATGAGCACTTTGGCATTGTCCC
TCTGGAAGCCATGTACATGCAGTGCCAGTCATTGCTGTTAATTTCGGGTGGACCCTTGGAGT
CCATTGACCACAGTGTACAGGGTTTCTGTGTGAGCCTGACCCGGTGCACCTTCTCAGAAGCA
ATAGAAAAGTTCATCCGTGAACCTTCCTTAAAAGCCACCATGGGCCTGGCTGGAAGAGCCAG
AGTGAAGGAAAAATTTTCCCCTGAAGCATTTACAGAACAGCTCTACCGATATGTTACCAAAC
TGCTGGTATTAATCAGATTGTTTTTAAAGATCTCCATTAATGTCATTTTTATGGATTGTAGACC
CAGTTTTGAAACCAAAAAAGAAACCTAGAATCTAATGCAGAAGAGATCTTTTAAAAAATAAA
CTTGAGTCTTGAATGTGAGCCACTTTCCTATATACCACACCTCCCTGTCCACTTTTCAGAAA
AACCATGTCTTTTATGCTATAATCATTCCAAATTTTGCCAGTGTTAAGTTACAAATGTGGTG
TCATTCCATGTTTCAGCAGAGTATTTTAATTATATTTTCTCGGGATTATTGCTCTTCTGTCTA
TAAATTTTGAATGATACTGTGCCTTAATTGGTTTTTCATAGTTTAAAGTGTGTATCATTATCAA
AGTTGATTAATTTGGCTTCATAGTATAATGAGAGCAGGGCTATTGTAGTTCCCAGATTCAAT
CCACCGAAGTGTTCACTGTCTGTTAGGGAATTTTTGTTTGTCTGTCTTTGCCTGGATC
CATAGCGAGAGTGCTCTGTATTTTTTTTTTAAAGATAATTTGTATTTTTTGCACACTGAGATATAA
TAAAAGGTGTTTATCATAAAAA

FIGURE 116

MPLLKLVHGSPLVFGEKFKLFTLVSACIPVFR LARRRKKILFYCHFPDLLLTKRDSFLKRLY
RAPIDWIEEYTTGMADCILVNSQFTA AVFKETFKSLSHIDPDVLYPSLNVTSFDSVVPEKLD
DLVPKGKKFLLLSINRYERKKNLTLALEALVQLRGRLTSQDWERVHLIVAGGYDERVLENVE
HYQELKKMVQQSDLGQYVTF LRSFSDKQKISLLHSCTCVLYTPSNEHFGIVPLEAMYMQCPV
IAVNSGGPLESIDHSVTGFLCEPDPVHFSEAIEKFIREPSLKATMGLAGRARVKEKFSPEAF
TEQLYRYVTKLLV

Signal peptide:

amino acids 1-15

FIGURE 117

GACTACGCCGATCCGAGACGTGGCTCCCTGGGCGGCAGAACCAATGTTGGACTTCGCGATCTT
CGCCGTTACCTTCTTGCTGGCGTTGGTGGGAGCCGTGCTCTACCTCTATCCGGCTTCCAGAC
AAGCTGCAGGAATTCAGGGATTACTCCAAGTGAAGAAAAAGATGGTAATCTTCCAGATATT
GTGAATAGTGGAAGTTTGCATGAGTTCCTGGTTAATTTGCATGAGAGATATGGGCCTGTGGT
CTCCTTCTGGTTTGGCAGGCGCCTCGTGGTTAGTTTGGGCACTGTTGATGTACTGAAGCAGC
ATATCAATCCCAATAAGACATCGGACCCTTTTGAAACCATGCTGAAGTCATTATTAAGGTAT
CAATCTGGTGGTGGCAGTGTGAGTGAAAACCATGAGGAAAAAATTGTATGAAAATGGTGT
GACTGATTCTCTGAAGAGTAACTTTGCCCTCCTCCTAAAGCTTTCAGAAGAATTATTAGATA
AATGGCTCTCCTACCCAGAGACCCAGCACGTGCCCCTCAGCCAGCATATGCTTGGTTTTGCT
ATGAAGTCTGTTACACAGATGGTAATGGGTAGTACATTTGAAGATGATCAGGAAGTCATTCG
CTTCAGAGAAGATCATGGCACAGTTTGGTCTGAGATTGGAAAAGGCTTCTAGATGGGTAC
TTGATAAAAACATGACTCGGAAAAACAATATGAAGATGCCCTCATGCAACTGGAGTCTGTT
TTAAGGAACATCATAAAAGAACGAAAAGGAAGGAACCTTCAGTCAACATATTTTCATTGACTC
CTTAGTACAAGGGAACCTTAATGACCAACAGATCCTAGAAGACAGTATGATATTTTCTCTGG
CCAGTTGCATAATAACTGCAAAATTGTGTACCTGGGCAATCTGTTTTTTAACCACCTCTGAA
GAAGTTCAAAAAAATTATATGAAGAGATAAACCAAGTTTTTGGAAATGGTCCTGTTACTCC
AGAGAAAATTGAGCAGCTCAGATATTGTGAGCATGTGCTTTGTGAACTGTTGAACTGCCA
AACTGACTCCAGTTTCTGCCCAGCTTCAAGATATTGAAGGAAAAATTGACCGATTTATTATT
CCTAGAGAGACCCTCGTCCTTTATGCCCTTGGTGTGGTACTTCAGGATCCTAATACTTGGCC
ATCTCCACACAAGTTTGATCCAGATCGGTTTGATGATGAATTAGTAATGAAAACCTTTTCCT
CACTTGGATTCTCAGGCACACAGGAGTGTCCAGAGTTGAGGTTTGCATATATGGTGACCACA
GTACTTCTTAGTGTATTGGTGAAGAGACTGCACCTACTTTCTGTGGAGGGACAGGTTATTGA
AACAAAGTATGAACTGGTAACATCATCAAGGGAAGAAGCTTGGATCACTGTCTCAAAGAGAT
ATTAAAATTTTATACATTTAAAATCATTGTTAAATTGATTGAGGAAAACAACCATTTAAAAA
AAATCTATGTTGAATCCTTTTATAAACAGTATCACTTTGTAATATAAACACCTATTTGTAC
TTAA

FIGURE 118

MLDFAIFAVTFLALVGAVLYLYPASRQAAGIPGITPTEEKDGNLPDIVNSGSLHEFLVNLH
ERYGPVVSFWFGRRLVVS LGTVDLKQHINPNKTS DPFETMLKSLRLRYQSGGGSVSENHMRK
KLYENGVTDSLKSNFALLLLKLSEELLDKWLSYPETQHVPLSQHMLGFAMKSVTQMVMGSTFE
DDQEVIRFQKNHGTWVSEIGKGFLDGSLDKNMTRKKQYEDALMQLESVLRNI IKERKGRNFS
QHIFIDSLVQGNLNDQQILED SMIFSLASCIITAKLCTWAICFLT TSEEVQKKLYEEINQVF
GNGPVTPEKIEQLRYCQHVL CETVRTAKLTPVSAQLQDIEGKIDRFIIPRET LVLYALGVVL
QDPNTWPSPHKFD PDRFDDEL VMKTFSSLGFSGTQECPELRFAYMVTTVLLSVLVKRLHLLS
VEGQVIETKYELVTSSREEAWITVSKRY

Signal peptide:

amino acids 1-18

Transmembrane domain:

amino acids 271-290

FIGURE 119

CTAGATTTGTCGGCTTGCGGGGAGACTTCAGGAGTCGCTGTCTCTGAACTTCCAGCCTCAGA
GACCGCCGCCCTTGTCCCCGAGGGCCATGGGCCGGGTCTCAGGGCTTGTGCCCTCTCGCTTC
CTGACGCTCCTGGCGCATCTGGTGGTCGTCATCACCTTATTCTGGTCCCGGGACAGCAACAT
ACAGGCCTGCCTGCCTCTCACGTTACCCCCGAGGAGTATGACAAGCAGGACATTCAGCTGG
TGGCCGCGCTCTCTGTCACCCTGGGCCTCTTTGCAGTGGAGCTGGCCGGTTTCCTCTCAGGA
GTCTCCATGTTCAACAGCACCCAGAGCCTCATCTCCATTGGGGCTCACTGTAGTGCATCCGT
GGCCCTGTCCTTCTTCATATTCGAGCGTTGGGAGTGCACCTACGTATTGGTACATTTTGTCT
TCTGCAGTGCCCTTCCAGCTGTCACTGAAATGGCTTTATTTCGTCACCGTCTTTGGGCTGAAA
AAGAAACCCTTCTGTATTACCTTCATGACGGGAACCTAAGGACGAAGCCTACAGGGGCAAGGG
CCGCTTCGTATTCCTGGAAGAAGGAAGGCATAGGCTTCGGTTTTCCCCTCGGAAACTGCTTC
TGCTGGAGGATATGTGTTGGAATAATTACGTCTTGAGTCTGGGATTATCCGCATTGTATTTA
GTGCTTTGTAATAAAATATGTTTTGTAGTAACATTAAGACTTATATACAGTTTTAGGGGACA
ATTAAAAAAAAAAAAA

FIGURE 120

MGRVSGLVPSRFLTLLAHLVVVITLFWSRDSNIQACLPLTFTPEEYDKQDIQLVAALSVTLG
LFAVELAGFLSGVSMFNSTQSLISIGAHCSASVALSFFIFERWECTTYWYIFVFCSALPAVT
EMALFVTVFGLKKKPF

Transmembrane domain:

amino acids 12-28 (type II), 51-66, 107-124

FIGURE 121

TCCCGGACCCTGCCGCCCTGCCACTATGTTCCCGCCGCTCTATGCTGCTTGCCTGGGCTCTCC
CCAGCCTCCTTCGACTCGGAGCGGCTCAGGAGACAGAAGACCCGGCCTGCTGCAGCCCCATA
GTGCCCCGGAACGAGTGGAAGGCCCTGGCATCAGAGTGCGCCACGACCTGAGCCTGCCCTT
ACGCTATGTGGTGGTATCGCACACGGCGGGCAGCAGCTGCAACACCCCCGCCTCGTGCCAGC
AGCAGGCCCGGAATGTGCAGCACTACCACATGAAGACACTGGGCTGGTGCACGTGGGCTAC
AACTTCCTGATTGGAGAAGACGGGCTCGTATACGAGGGCCGTGGCTGGAACCTTCACGGGTGC
CCACTCAGGTCACCTTATGGAACCCCATGTCCATTGGCATCAGCTTCATGGGCAACTACATGG
ATCGGGTGCCACACCCCAGGCCATCCGGGCAGCCCAGGGTCTACTGGCCTGCGGTGTGGCT
CAGGGAGCCCTGAGGTCCAACCTATGTGCTCAAAGGACACCGGGATGTGCAGCGTACACTCTC
TCCAGGCAACCAGCTCTACCACCTCATCCAGAATTGGCCACACTACCGCTCCCCCTGAGGGCC
CTGCTGATCCGCACCCCATTCCTCCCCTCCCATGGCCAAAAACCCCACTGTCTCCTTCTCCA
ATAAAGATGTAGCTC

FIGURE 122

MSRRSMLLAWALPSLLRLGAAQETEDPACCSPIVPRNEWKALASECAQHLSLPLRYVVSHT
AGSSCNTPASCQQQARNVQHYHMKT LGWCDVGYNFLIGEDGLVYEGRGWNFTGAHSGHLWNP
MSIGISFMGNYMDRVPTPQAIRAAQGLLACGVAQGALRSNYVLKGHRDVQRTLSPGNQLYHL
IQNWPHYRSP

Signal peptide:
amino acids 1-20

FIGURE 123

CTGGGACCCCGAAAAGAGAAGGGGAGAGCGAGGGGACGAGAGCGGAGGAGGAAGATGCAACT
GACTCGCTGCTGCTTCGTGTTCTGGTGCAGGGTAGCCTCTATCTGGTCATCTGTGGCCAGG
ATGATGGTCCTCCCGGCTCAGAGGACCCTGAGCGTGATGACCACGAGGGCCAGCCCCGGCCC
CGGGTGCCTCGGAAGCGGGGCCACATCTCACCTAAGTCCCGCCCCATGGCCAATTCCACTCT
CCTAGGGCTGCTGGCCCCGCCTGGGGAGGCTTGGGGCATTCTTGGGCAGCCCCCAACCGCC
CGAACCACAGCCCCCACCTCAGCCAAGGTGAAGAAATCTTTGGCTGGGGCGACTTCTAC
TCCAACATCAAGACGGTGGCCCTGAACCTGCTCGTCACAGGGAAGATTGTGGACCATGGCAA
TGGGACCTTCAGCGTCCACTTCCAACACAATGCCACAGGCCAGGGAAACATCTCCATCAGCC
TCGTGCCCCCAGTAAAGCTGTAGAGTTCCACCAGGAACAGCAGATCTTCATCGAAGCCAAG
GCCTCCAAAATCTTCAACTGCCGGATGGAGTGGGAGAAGGTAGAACGGGGCCGCQGGACCTC
GCTTTGCACCCACGACCCAGCCAAGATCTGCTCCCGAGACCACGCTCAGAGCTCAGCCACCT
GGAGCTGCTCCCAGCCCTTCAAAGTCGTCTGTGTCTACATCGCCTTCTACAGCACGGACTAT
CGGCTGGTCCAGAAGGTGTGCCCAGATTACAACCTACCATAGTGATACCCCTACTACCCATC
TGGGTGACCCGGGGCAGGCCACAGAGGCCAGGCCAGGGCTGGAAGGACAGGCCTGCCCCATGC
AGGAGACCATCTGGACACCGGGCAGGGAAGGGGTTGGGCCTCAGGCAGGGAGGGGGGTGGAG
ACGAGGAGATGCCAAGTGGGGCCAGGGCCAAGTCTCAAGTGGCAGAGAAAGGGTCCCAAGTG
CTGGTCCCAACCTGAAGCTGTGGAGTGACTAGATCACAGGAGCACTGGAGGAGGAGTGGGCT
CTCTGTGCAGCCTCACAGGGCTTTGCCACGGAGCCACAGAGAGATGCTGGGTCCCCGAGGCC
TGTGGGCAGGCCGATCAGTGTGGCCCCAGATCAAGTCATGGGAGGAAGCTAAGCCCTTGGTT
CTTGCCATCCTGAGGAAAGATAGCAACAGGGAGGGGGAGATTTTCATCAGTGTGGACAGCCTG
TCAACTTAGGATGGATGGCTGAGAGGGCTTCCTAGGAGCCAGTCAGCAGGGTGGGGTGGGGC
CAGAGGAGCTCTCCAGCCCTGCCTAGTGGGCGCCCTGAGCCCCTTGTCGTGTGCTGAGCATG
GCATGAGGCTGAAGTGGCAACCCTGGGGTCTTTGATGTCTTGACAGATTGACCATCTGTCTC
CAGCCAGGCCACCCCTTTCCAAAATTCCCTCTTCTGCCAGTACTCCCCCTGTACCACCCATT
GCTGATGGCACACCCATCCTTAAGCTAAGACAGGACGATTGTGGTCCTCCCACACTAAGGCC
ACAGCCCATCCGCGTGCTGTGTGTCCCTCTTCCACCCCAACCCCTGCTGGCTCCTCTGGGAG
CATCCATGTCCCGGAGAGGGGTCCCTCAACAGTCAGCCTCACCTGTCAGACCGGGGTCTCC
CGGATCTGGATGGCGCCGCCCTCTCAGCAGCGGGCACGGGTGGGGCGGGGCCGGGCCGAGA
GCATGTGCTGGATCTGTTCTGTGTGTCTGTCTGTGGGTGGGGGAGGGGAGGGAAGTCTTGT
GAAACCGCTGATTGCTGACTTTTGTGTGAAGAATCGTGTTCTTGGAGCAGGAAATAAAGCTT
GCCCCGGGGCA

FIGURE 124

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA66521

><subunit 1 of 1, 252 aa, 1 stop

><MW: 28127, pI: 8.91, NX(S/T): 5

MLTRCCFVFLVQGSLLVICGQDDGPPGSEDPERDDHEGQPRPRVPRKRGHISPKSRPMAN
STLLGLLAPPGEAWGILGQPPNRPNHSPPPSAKVKKIFGWGDFYSNIKTVALNLLVTGKIVD
HGNGTFSVHFQHNATGQGNISISLVPPSKAVEFHQEQQIFIEAKASKIFNCRMEWEKVERGR
RTSLCTHDPAKICSRDHAQSSATWSCSQPFKVVCVYIAFYSTDYRLVQKVCPDYNHSDTPY
YPSG

Important features of the protein:

Signal peptide:

amino acids 1-14

N-glycosylation sites.

amino acids 62-65, 127-130, 137-140, 143-146

2-oxo acid dehydrogenases acyltransferase

amino acids 61-71

FIGURE 125

GTGAATGTGAGGGTTTGATGACTTTTCTAGGAACCAGAGTGGGTGCAGGGGCCCCA
GGCAGGGCTGATTCTTGGGCGGAGGAGAGTAGGGTAAAGGGTTCTGCATGAGCTCCTTAAAG
GACAAAGGTAACAGAGCCAGCGAGAGAGCTCGAGGGGAGACTTTGACTTCAAGCCACAGAAT
TGGTGGAAAGTGTGCGCGCCGCCGCCGCGTCTGCTCCTGCAGCGCTGTCGACCTAGCCGCTAG
CATCTTCCCCGAGCACCGGGATCCCCGGGGTAGGAGGCGACGCGGGCGAGCACCAGCGCCAGCC
GGCTGCGGCTGCCCACACGGCTCACCATGGGGCTCCGGGCGCCGGGCGCTGTCCGCGGTGCCG
GCCGTGCTGCTGGTCTTACGCTGCCGGGGCTGCCCGTCTGGGCACAGAACGACACGGAGCC
CATCGTGCTGGAGGGCAAGTGTCTGGTGGTGTGCGACTCGAACC CGGCCACGGACTCCAAGG
GCTCCTCTTCTCCCCGCTGGGGATATCGGTCCGGGCGGCCAACTC CAAGTCTCGCTTCTCG
GCGGTGCGGAGCACCAACCACGAGCCATCCGAGATGAGCAACAAGACGCGCATCATTTACTT
CGATCAGATCCTGGTGAATGTGGGTAAATTTTTTACATTGGAGTCTGTCTTTGTAGCACCAA
GAAAAGGAATTTACAGTTTTCAGTTTTTACGTGATTAAAGTCTACCAGAGCCAACTATCCAG
GTTAACTTGATGTTAAATGGA AAACCAGTAATATCTGCCTTTGCGGGGGACAAAGATGTTAC
TCGTGAAGCTGCCACGAATGGTGTCTGCTCTACCTAGATAAAGAGGATAAGGTTTACCTAA
AACTGGAGAAAGGTAATTTGGTTGGAGGCTGGCAGTATTCCACGTTTTCTGGCTTTCTGGTG
TTCCCCCTATAGGATTCAATTTCTCCATGATGTTTATCCAGGTGAGGGATGACCCACTCCTG
AGTTATTGGAAGATCATTTTTTTCATCATTGGATTGATGTCTTTTATTGGTTTCTCATGGGTG
GATATGGATTCTAAGGATTCTAGCCTGTCTGAACCAATACAAAATTTACAGATTATTTGTG
TGTGTCTGTTTCAGTATATTTGGATTGGGACTCTAAGCAGATAATACCTATGCTTAAATGTA
ACAGTCAAAAGCTGTCTGCAAGACTTATTCTGAATTTTCAATTCCTGGGATTACTGAATTAGT
TACAGATGTGGAATTTTATTTGTTTAGTTTTTAAAAGACTGGCAACCAGGTCTAAGGATTAGA
AACTCTAAAGTTCTGACTTCAATCAACGGTTAGTGTGATACTGCCAAAGAACTGTATACTG
TGTTAATATATTGATTATATTTGTTTTTATTCCTTTGGAATTAGTTTGTTTGGTTCTTGTA
AAAATTTGGATTTTTTTTTTTTTCAGTAACTGGTATTATGTTTTCTCTTAAAATAAGGTAATGAA
TGGCTTGCCACAAATTTACCTTGACTACGATATCATCGACATGACTTCTCTCAAAAAAAAA
GAATGCTTCATAGTTGTATTTTAATTGTATATGTGAAAGAGTCATATTTTCCAAGTTATATT
TTCTAAGAAGAAGAATAGATCATAAATCTGACAAGGAAAAAGTTGCTTACCCAAAATCTAAG
TGCTCAATCCCTGAGCCTCAGCAAAACAGCTCCCCTCCGAGGGAAATCTTATACTTTATTGC
TCAACTTTAATTAATAATGATTGATAATAACCACTTTATTAAAAACCTAAGGTTTTTTTTTT
TCCGTAGACATGACCACTTTATTAACCTGGTGGTGGGATGCTGTTGTTTCTAATTATACCTAT
TTTTCAAGGCTTCTGTTGTATTTGAAGTATCATCTGGTTTTGCCTTAACTCTTTAAATTGTA
TATATTTATCTGTTTAGCTAATATTAAATTCAAATATCCCATATCTAAATTTAGTGCAATAT
CTTGTCTTTTGTATAGGTCATATGAATTCATAAAATTATTTATGTCTGTTATAGAATAAAGA
TTAATATATGTTAAAAAAA

FIGURE 126

MSGRRALSAVPAVLLVLTLPGLPVWAQNDTEPIVLEGKCLVVCDSNPATDSKGSSSSPLGI
SVRAANSKVAFSAVRSTNHEPSEMSNKTRIIYFDQILVNVGNFFTLESV FVAPRKGIIYSFSF
HVIKVYQSQTIQVNLMLNGKPVISAFAGDKDVTREAAATNGVLLYLDKEDKVYLKLEKGNLVG
GWQYSTFSGFLVFPL

Signal peptide:

amino acids 1-27

FIGURE 127

CGGTGGCCATGACTGCGGCCGTGTTCTTCGGCTGCGCCTTCATTGCCTTCGGGCCTGCGCTC
GCCCTTTATGTCTTCACCATCGCCATCGAGCCGTTGCGTATCATCTTCCTCATCGCCGGAGC
TTTCTTCTGGTTGGTGTCTCTACTGATTTTCGTCCCTTGTTTGGTTCATGGCAAGAGTCATTA
TTGACAACAAAGATGGACCAACACAGAAATATCTGCTGATCTTTGGAGCGTTTGTCTCTGTC
TATATCCAAGAAATGTTCCGATTTGCATATTATAAACTCTTAAAAAAGCCAGTGAAGGTTT
GAAGAGTATAAACCAGGTGAGACAGCACCCCTCTATGCGACTGCTGGCCTATGTTTCTGGCT
TGGGCTTTGGAATCATGAGTGGAGTATTTTCCTTTGTGAATACCCTATCTGACTCCTTGGGG
CCAGGCACAGTGGGCATTATGAGATTCTCCTCAATTCTTCCTTTATTCAGCTTTCATGAC
GCTGGTCATTATCTTGCTGCATGTATTCTGGGGCATTGTATTTTTTGATGGCTGTGAGAAGA
AAAAGTGGGGCATCCTCCTTATCGTTCTCCTGACCCACCTGCTGGTGTGAGCCCAGACCTTC
ATAAGTTCTTATTATGGAATAAACCTGGCGTCAGCATTTATAATCCTGGTGCTCATGGGCAC
CTGGGCATTCTTAGCTGCGGGAGGCAGCTGCCGAAGCCTGAAACTCTGCCTGCTCTGCCAAG
ACAAGAACTTTCTTCTTTACAACCAGCGCTCCAGATTAACCTCAGGGAACCAGCACTTCCCAA
ACCGCAGACTACATCTTTAGAGGAAGCACAACTGTGCCTTTTTCTGAAAATCCCTTTTTCTG
GTGGAATTGAGAAAGAAATAAACTATGCAGATA

FIGURE 128

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA66658

><subunit 1 of 1, 257 aa, 1 stop

><MW: 28472, pI: 9.33, NX(S/T): 0

MTAAVFFGCAFIAGFPALALYVFTIAIEPLRIIFLIAGAFFWLVSLLISSLVWFMARVIIDN
KDGPTQKYLLIFGAFVSVYIQEMFRFAYYKLLKKASEGLKSINPGETAPSMRLLAYVSGLGF
GIMSGVFSFVNTLSDSLPGTVGIHGDSPQFFLYSAFMTLVIIILLHVFWGIVFFDGCEKKKW
GILLIVLLTHLLVSAQTFISSYYGINLASAFIILVLMGTWAF LAAGGSCRSLKLCCLLCQDKN
FLLYNQSR

Important features of the protein:

Signal peptide:

amino acids 1-19

Transmembrane domains:

amino acids 32-51, 119-138, 152-169, 216-235

Glycosaminoglycan attachment site.

amino acids 120-123

Sodium:neurotransmitter symporter family protein

amino acids 31-65

FIGURE 129

CGGCAACCAGCCGCCGCCACCACCGCTGCCACTGCCGCCCTGCCGGGGCCATGTTCTGCTCTGGGCTTGCCCTTCT
TGGTGTCTTGGTGGCCTCGGTGAGAGCCATCTGGGGGTTCTGGGGCCCAAGAACGTCTCGCAGAAAGACGCCG
AGTTTGAGCGCACCTACGTGGACGAGGTCAACAGCGAGCTGGTCAACATCTACACCTTCAACCATACTGTGACCC
GCAACAGGACAGAGGGCGTGGCTGTGTCTGTGAACGTCTGAACAAGCAGAAGGGGGCGCCGTGCTGTTTGTGG
TCCGCCAGAAGGAGGCTGTGGTGTCTTCCAGGTGCCCTAATCCTGCGAGGGATGTTTTCAGCGCAAGTACCTCT
ACCAAAAGTGGAAACGAACCTGTGTGAGCCCCCACCAGAATGAGTCGGAGATTGAGTTCTTCTACGTGGATG
TGTCACCCCTGTCAACAGTCAACACCACATACCAGCTCCGGGTGAGCCGCATGGACGATTTTGTGCTCAGGACTG
GGGAGCAGTTTCACTTCAATACCACAGCAGCACAGCCCCAGTACTTCAAGTATGAGTTCCCTGAAGGCGTGGACT
CGGTAATTGTCAAGGTGACCTCCAACAAGGCCTTCCCTGCTCAGTCATCTCCATTGAGGATGTGCTGTGCTGCTG
TCTATGACCTGGACAACAACGTAGCCTTTCATCGGCATGTACCAGACGATGACCAAGAAGCGGCCATCACCGTAC
AGCGCAAAGACTTCCCCAGCAACAGCTTTATGTGGTGGTGGTGAAGACCGAAGACCAAGCCTGCGGGGGCT
CCCTGCCTTTCTACCCCTTCGCAGAAGATGAACCGGTGATCAAGGGCACCAGCCAGAAAACCTGTGAGTGTGG
TGTCTCAAGCAGTCACGTCTGAGGCATACGTGAGTGGGATGCTCTTTTGGCTGGGTATATTTCTCTCTTTTACC
TGCTGACCGTCTCTGCGCTGCTGGGAGAACTGGAGGCAGAAGAAGAAGACCTGCTGGTGGCCATTGACCGAG
CCTGCCAGAAAGCGGTACCCCTCGAGTCTGGCTGATTCTTTTCTGGCAGTTCCCTTATGAGGGTTACAACCT
ATGGCTCTTTTGAGAATGTTTCTGGATCTACCGATGGTCTGGTTGACAGCGCTGGCACTGGGGACCTCTCTTACG
GTTACCAGGGCCGCTCTTTGAACCTGTAGGTACTCGGCCCGAGTGGACTCCATGAGCTCTGTGGAGGAGGATG
ACTACGACACATTGACCGACATCGATTCCGACAAGAATGTCAATTCGCACCAAGCAATACCTCTATGTGGCTGACC
TGGCAGCGAAGGACAAGCGTGTCTGCGGAAAAAGTACCAGATCTACTTCTGGAACATTGCCACCATTGCTGTCT
TCTATGCCCTTCTGTGGTGCAGCTGGTGTATCCTACCAGACGGTGGTGAATGTACAGGGAATCAGGACATCT
GCTACTACAACCTCTCTGCGCCACCCACTGGGCAATCTCAGCGCTTCAACAACATCCTCAGCAACCTGGGGT
ACATCTGCTGGGGCTGCTTTTCTGCTCATCATCTGCAACGGGAGATCAACCACAACCGGGCCCTGCTGCGCA
ATGACCTCTGTGCCCTGGAATGTGGGATCCCCAAACACTTTGGGCTTTTCTAGCCATGGGCACAGCCCTGATGA
TGGAGGGGCTGCTCAGTGCTTGCTATCATGTGTGCCCCAACTATACCAATTTCCAGTTTGACACATCGTTCATGT
ACATGATCGCCGACTCTGCATGCTGAAGCTCTACCAGAAGCGGCACCCGGACATCAACGCCAGCGCCTACAGTG
CCTACGCCCTGCTGGCCATTGTCTATCTTCTCTGTGCTGGGCGTGGTCTTTGGCAAAGGGAACACGGCGTTCT
GGATCGTCTTCTCATCATTCACATCATCGCCACCCTGCTCCTCAGCACGCAGCTCTATTACATGGGCGGTGGA
AACTGGACTCGGGGATCTTCCGCGCATCTCCACGTGCTCTACACAGACTGCATCCGGCAGTGCAGCGGGCCGC
TCTACGTGGACCGCATGGTGTGCTGGTGTGTCATGGGCAACGTCACTCAACTGGTCTGCTGGCTGCTATGGGCTTATCA
TGCGCCCCAATGATTTGCTTCTACTTGTGGCCATTGGCATCTGCAACCTGCTCCTTTACTTTCGCTTCTACA
TCATCATGAAGTCCCGAGTGGGGAGAGGATCAAGCTCATCCCCCTGCTCTGCATCGTTTGACCTCCGTGGTCT
GGGGCTTCGCGCTCTTCTTCTTCTTCCAGGACTCAGCACCTGGCAGAAAACCCCTGCAGAGTTCGAGGGAGCACA
ACCGGACTGCATCTCTCGACTTCTTTGACGACCACGACATCTGGCACTTCTCTCTCCATCGCCATGTTTCG
GGTCTTCTGGTGTGTGCTGACACTGGATGACGACCTGGATACTGTGCAGCGGACAAGATCTATGTCTTCTAGC
AGGAGCTGGGCCCTTCGCTTCACTTCAAGGGGCCCTGAGCTCCTTGTGTCTAGACCGGTCACTCTGTGCTGCT
GTGGGATGAGTCCCAGCACCGCTGCCAGCACTGGATGGCAGCAGGACAGCCAGGTCTAGCTTAGGCTTGGCCT
GGGACAGCCATGGGGTGGCATGGAACCTTGCAGCTGCCCTCTGCCAGGAGCAGGCCTGCTCCCTGGAACCCCC
AGATGTTGGCCAAATTGCTGCTTCTTCTCAGTGTGGGGCTTCCATGGGGCCCTGCTCTTGGCTCTCCATTT
GTCCCTTTGCAAGAGGAAGGATGGAAGGGACACCTCCCCATTTGATGCTTGCATTTTGGCCGCTCTCTCCCC
ACAAATGCCCCAGCCTGGGACCTAAGGCCTCTTTTCTCTCCATACTCCCACTCCAGGGCCTAGTCTGGGGCTGA
ATCTCTGTCTGTATCAGGGCCCCAGTTCTTTGGGCTGTCCCTGGCTGCCATCACTGCCATTCCAGTCAGCC
AGGATGGATGGGGGTATGAGATTTGGGGGTGGCCAGCTGGTGGCAGACTTTTGGTGTAAAGGCTGCAAGGGG
CCTGGGGCAGTGCATTTCTTCTTCTGACCTGTGCTCAGGGCTGGCTCTTTAGCAATGCGCTCAGCCCAATT
TGAGAACCGCTTCTGATTCAAGAGGCTGAATTCAGAGGTCACCTCTTCATCCCATCAGCTCCAGACTGATGCC
AGCACCAGGACTGGAGGGAGAAGCGCCTCACCCCTTCCCTTCTTCTTCCAGGCCCTTAGTCTTGCCAAACCCC
AGCTGGTGGCCTTTCAGTGCCATTGACACTGCCCCAAGAATGTCCAGGGGCAAGGAGGGATGATACAGAGTTCAG
CCGTTCTGCCTCCACAGCTGTGGGCACCCAGTGCCTACCTTAGAAAGGGGCTTCAGGAAGGGATGTGCTGTTT
CCCTTACGTGCCAGTCTTAGCCTCGCTTAGGACCCAGGGCTGGCTTCTAAGTTTCCGTCCAGTCTTCAGGCA
AGTTCTGTGTTAGTCATGCACACATACCTATGAAACCTTGGAGTTTACAAAGAATTGCCCCAGCTCTGGGCAC
CCTGGCCACCCCTGGTCTTGGATCCCCTTCGTCCCACCTGGTCCACCCAGATGCTGAGGATGGGGGAGCTCAGG
CGGGGCTCTGCTTGGGGATGGGAATGTGTTTTCTCCAAACTGTTTTTATAGCTCTGCTTGAAGGGCTGGG
AGATGAGGTGGTCTGGATCTTTTCTCAGAGCGTCTCCATGCTATGGTTGCATTTCCGTTTTCTATGAATGAATT
TGCATTCAATAACAACAGACTCAAAAAAAAAAAAAA

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FIGURE 130

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA66659
><subunit 1 of 1, 832 aa, 1 stop
><MW: 94454, pI: 6.94, NX(S/T): 12
MFALGLPFLVLLVASVESH LGVLGPKNVSQKDAEFERTYVDEVNSELVNIYTFNHTVTRNRT
EGVRVSVNVLNKQKGAPLLFVVRQKEAVVSFQVPLILRGMFQRKYLYQKVERTLCQPPTKNE
SEIQFFYVDVSTLSPVNTTYQLRVSRMDDFVLR TGEQFSFNTTAAQEQYFKYEFPEGVD SVI
VKVTSNKAFFPCSVISIQDVLCPVYDLN NVAFIGMYQTMTKKAAITVQRKDFPSNSFYVVVV
VKTEDQACGGSLPFYPFAEDEPVDQGHRQKTL SVLVSQAVTSEAYVSGMLFCLGIFLSFYLL
TVLLACWENWRQKKKTLLVAIDRACPESGHPRVLADSFPGSSPYEGYNYGSFENVSGSTDGL
VDSAGTGDLSYGYQGRSFEPVGTRPRVDSMSSVEEDDYDTLTDIDSDKNVIRTKQYLYVADL
ARKDKRVLRRKKYQIYFWNIATIAVFYALPVVQLVITYQTVVNVVTGNQDICYNFLCAHPLGN
LSAFNNILSNLGYILLGLLFLLIILQREINHNRALLRNDLCALECGIPKHFGFLFYAMGTALM
MEGLLSACYHVC PN YTNFQFDT SFMYMIAGLCMLKLYQKRHPDINASAYSAYACLAIVIFFS
VLGVVFGKGNTAFWIVFSIIHIIATLLLSTQLYYMGRWKLD SGIFRRILHVLYTDCIRQCSG
PLYVDRMVLLVMGNVINWSLAAYGLIMRPNDFASYLLAIGICNLLLYFAFYIIMKLRSGERI
KLIPLLCIVCTSVVWGFALFFFQQLSTWQKTPAESREHNRDCILLDFDDHDIWHFLSSIA
MFGSFLVLLTLDDDLDTVQRDKIYVF

Important features of the protein:**Signal peptide:**

amino acids 1-18

Transmembrane domains:

amino acids 292-317, 451-470, 501-520, 607-627, 751-770

Leucine zipper pattern.

amino acids 497-518

N-glycosylation sites.amino acids 27-30, 54-57, 60-63, 123-126, 141-144, 165-168, 364-
367, 476-479, 496-499, 572-575, 603-606, 699-702

FIGURE 131

GCTCAAGTGCCTTGCCCTGCCCCACCCAGCCCAGCCTGGCCAGAGCCCCCTGGAGAAGGAGC
TCTCTTCTTGCTTGGCAGCTGGACCAAGGGAGCCAGTCTTGGGCGCTGGAGGGCCTGTCTTG
ACCATGGTCCCTGCCTGGCTGTGGCTGCTTTGTGTCTCCGTCCCCAGGCTCTCCCCAAGGC
CCAGCCTGCAGAGCTGTCTGTGGAAGTTCCAGAAAATATGGTGGAAATTTCCCTTTATACC
TGACCAAGTTGCCGCTGCCCCGTGAGGGGGCTGAAGGCCAGATCGTGCTGTGAGGGGACTCA
GGCAAGGCAACTGAGGGCCCATTGTCTATGGATCCAGATTCTGGCTTCCTGTGGTGACCAG
GGCCTGGACCGAGAGGAGCAGGCAGAGTACCAGCTACAGGTACCCCTGGAGATGCAGGATG
GACATGTCTTGTGGGGTCCACAGCCTGTGCTTGTGCACGTGAAGGATGAGAATGACCAGGTG
CCCCATTTCTCTCAAGCCATCTACAGAGCTCGGCTGAGCCGGGGTACCAGGCCTGGCATCCC
CTTCCTCTTCCCTGAGGCTTCAGACCGGGATGAGCCAGGCACAGCCAACTCGGATCTTCGAT
TCCACATCCTGAGCCAGGCTCCAGCCCAGCCTTCCCCAGACATGTTCCAGCTGGAGCCTCGG
CTGGGGGCTCTGGCCCTCAGCCCCAAGGGGAGCACCAGCCTTGACCACGCCCTGGAGAGGAC
CTACCAGCTGTTGGTACAGGTCAAGGACATGGGTGACCAGGCCTCAGGCCACCAGGCCACTG
CCACCGTGGAAGTCTCCATCATAGAGAGCACCTGGGTGTCCCTAGAGCCTATCCACCTGGCA
GAGAATCTCAAAGTCTTATACCCGCACCACATGGCCCAGGTACACTGGAGTGGGGGTGATGT
GCACTATCACCTGGAGAGCCATCCCCCGGGACCCTTTGAAGTGAATGCAGAGGGAAACCTCT
ACGTGACCAGAGAGCTGGACAGAGAAGCCAGGCTGAGTACCTGCTCCAGGTGCGGGCTCAG
AATTCCCATGGCGAGGACTATGCGGGCCCTCTGGAGCTGCACGTGCTGGTGATGGATGAGAA
TGACAACGTGCCTATCTGCCCTCCCCGTGACCCACAGTCAGCATCCCTGAGCTCAGTCCAC
CAGGTACTGAAGTGAAGTACTGTGTCAGCAGAGGATGCAGATGCCCCCGGCTCCCCCAATTCC
CACGTTGTGTATCAGCTCCTGAGCCCTGAGCCTGAGGATGGGGTAGAGGGGAGAGCCTTCCA
GGTGGACCCCACTTCAGGCAGTGTGACGCTGGGGGTGCTCCCACTCCGAGCAGGCCAGAACA
TCCTGCTTCTGGTGCTGGCCATGGACCTGGCAGGCGCAGAGGGTGGCTTCAGCAGCACGTGT
GAAGTCGAAGTCGCAGTCACAGATATCAATGATCACGCCCCCTGAGTTCATCACTTCCAGAT
TGGGCCTATAAGCCTCCCTGAGGATGTGGAGCCCGGGACTCTGGTGGCCATGCTAACAGCCA
TTGATGCTGACCTCGAGCCCGCCTTCCGCCTCATGGATTTTGCCATTGAGAGGGGAGACACA
GAAGGGACTTTTGGCCTGGATTGGGAGCCAGACTCTGGGCATGTTAGACTCAGACTCTGCAA
GAACCTCAGTTATGAGGCAGCTCCAAGTCATGAGGTGGTGGTGGTGGTGAGAGTGTGGCGA
AGCTGGTGGGGCCAGGCCCAGGCCCTGGAGCCACCGCCACGGTGACTGTGCTAGTGGAGAGA
GTGATGCCACCCCCCAAGTTGGACCAGGAGAGCTACGAGGCCAGTGTCCCATCAGTGCCCC
AGCCGGCTCTTTCCTGCTGACCATCCAGCCCTCCGACCCCATCAGCCGAACCCCTCAGGTTCT
CCCTAGTCAATGACTCAGAGGGCTGGCTCTGCATTGAGAAATTTCTCCGGGGAGGTGCACACC
GCCCAGTCCCTGCAGGGCGCCAGCCTGGGGACACCTACACGGTGCTTGTGGAGGCCCAGGA
TACAGCCCTGACTCTTGCCCCTGTGCCCTCCCAATACCTCTGCACACCCCGCCAAGACCATG
GCTTGATCGTGAGTGGACCCAGCAAGGACCCGATCTGGCCAGTGGGCACGGTCCCTACAGC
TTCACCCTTGGTCCCAACCCACGGTGCAACGGGATTGGCGCCTCCAGACTCTCAATGGTTTC
CCATGCCTACCTACCTTGGCCCTGCATTGGGTGGAGCCACGTGAACACATAATCCCCGTGG
TGGTCAGCCACAATGCCAGATGTGGCAGCTCCTGGTTGAGTGATCGTGTGTGCTGCTGCAAC
GTGGAGGGGAGTGATGCGCAAGGTGGGCGCATGAAGGGCATGCCCACGAAGCTGTGCGC
AGTGGGCATCCTTGATAGGCACCCTGGTAGCAATAGGAATCTTCCTCATCCTCATTTTACCC
ACTGGACCATGTCAAGGAAGAAGGACCCGGATCAACCAGCAGACAGCGTGCCCTGAAGGCG
ACTGTCTGAATGGCCCAGGCAGCTCTAGCTGGGAGCTTGGCCTCTGGCTCCATCTGAGTCCC
CTGGGAGAGAGCCCAGCACCCAAGATCCAGCAGGGGACAGGACAGAGTAGAAGCCCCCTCCAT
CTGCCCTGGGGTGGAGGCACCATCACCATCACAGGCATGTCTGCAGAGCCTGGACACCAAC
TTTATGGACTGCCCATGGGAGTGCTCCAAATGTCAGGGTGTGTTGCCCAATAATAAAGCCCCA
GAGAACTGGGCTGGGCCCTATGGGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAG

FIGURE 132

MVPAWLWLLCVSVPQALPKAQAELSVEVPENYGGNFPLYLTKLPLPREGAEGQIVLSGDSG
KATEGPFAMDPDSGFLLVTRALDREEQA EYQLQVTLEMQDGHVLWGPQPVLVHVKDENDQVP
HFSQAIYRARLSRGTRPGIPFLFLEASDRDEPGTANSDLRFHILSQAPAQSPDMFQLEPRL
GALALSPKGSTSLDHALERTYQLLVQVKMDGDQASGHQATATVEVSI IESTWVSLEPIHLAE
NLKVLYPHMAQVHWSGGDVHYHLESHPPGPFEVNAEGNLYVTRELDREAQAEYLLQVRAQN
SHGEDYAAPLELHVLVMDENDNVPICPPRDPTVSIPELSPPGTEVTRLAEDADAPGSPNSH
VVYQLLSPEPEDGVEGRAFQVDPTSGSVTLGVLPLRAGQNILLVLAMDLAGAEGGFSSTCE
VEVAVTDINDHAPEFITSQIGPISLPEDVEPGTLVAMLT AIDADLEPAFRLMDFAIERGDTE
GTFGLDWEPSDGHVRLRLCKNLSYEAAPSHEVVVVVQSVAKLVGPGPGPGATATVTVLVERV
MPPPKLDQESYEASVPISAPAGSFLLTIQPSDPI SRTLRFSLVNDSEGWLCIEKFSGEVHTA
QSLQGAQPGDTYTVLVEAQDTALT LAPVPSQYLCTPRQDHGLIVSGPSKDPDLASGHGPYSF
TLGPNPTVQRDWRLQTLNGSHAYLTLALHWVEPREHIIPVVVSHNAQMWQLLVRVIVCRCNV
EGQCMRKVGRMKGMPTKLSAVGILVGT LVAIGIFLILIFTHWTMSRKKDPDQPADSVPLKATV

Signal peptide:

amino acids 1-18

Transmembrane domain:

amino acids 762-784

FIGURE 133

CCGGGGACATGAGGTGGATACTGTTTCATTGGGGCCCTTATTGGGTCCAGCATCTGTGGCCAA
GAAAAATTTTTTGGGGACCAAGTTTTGAGGATTAATGTCAGAAATGGAGACGAGATCAGCAA
ATTGAGTCAACTAGTGAATTCAAACAACCTGAAGCTCAATTTCTGGAAATCTCCCTCCTCCT
TCAATCGGCCCTGTGGATGTCTGGTCCCCTCTGTCTGAGTCTGCAGGCATTTAAATCCTTCCTG
AGATCCCAGGGCTTAGAGTACGCAGTGACAATTGAGGACCTGCAGGCCCTTTTAGACAATGA
AGATGATGAAATGCAACACAATGAAGGGCAAGAACGGAGCAGTAATAACTTCAACTACGGGG
CTTACCATTCCCTGGAAGCTATTTACCACGAGATGGACAACATTGCCGCAGACTTTCTGAC
CTGGCGAGGAGGGTGAAGATTGGACATTCGTTTGAAAACCGGCCGATGTATGTACTGAAGTT
CAGCACTGGGAAAGGCGTGAGGCGGCCGGCCGTTTGGCTGAATGCAGGCATCCATTCCCGAG
AGTGGATCTCCCAGGCCACTGCAATCTGGACGGCAAGGAAGATTGTATCTGATTACCAGAGG
GATCCAGCTATCACCTCCATCTTGGAGAAAATGGATATTTTCTTGTGCTGTGGCCAATCC
TGATGGATATGTGTATACTCAAACCTCAAACCGATTATGGAGGAAGACGCGGTCCCGAAATC
CTGGAAGCTCCTGCATTGGTGTGACCCAAATAGAACTGGAACGCTAGTTTGCAGGAAAG
GGAGCCAGCGACAACCTTGCTCCGAAGTGTACCATGGACCCACGCCAATTCGGAAGTGGA
GGTGAATCAGTGGTAGATTTTCATCCAAAACATGGGAATTTCAAGGGCTTCATCGACCTGC
ACAGCTACTCGCAGCTGCTGATGTATCCATATGGGTACTCAGTCAAAAAGGCCCCAGATGCC
GAGGAACTCGACAAGGTGGCGAGGCTTGCGGCCAAAGCTCTGGCTTCTGTGTGCGGCACTGA
GTACCAAGTGGGTCCACCTGCACCACTGTCTATCCAGCTAGCGGAGCAGCATCGACTGGG
CGTATGACAACGGCATCAAATTTGCATTACATTTGAGTTGAGAGATACCGGGACCTATGGC
TTCCTCCTGCCAGCTAACCAGATCATCCCCACTGCAGAGGAGACGTGGCTGGGGCTGAAGAC
CATCATGGAGCATGTGCGGGACAACCTCTACTAGGCGATGGCTCTGCTCTGTCTACATTTAT
TTGTACCCACACGTGCACGCACTGAGGCCATTGTTAAAGGAGCTCTTTCCTACCTGTGTGAG
TCAGAGCCCTCTGGGTTTGTGGAGCACACAGGCCTGCCCCCTCTCCAGCCAGCTCCCTGGAGT
CGTGTGTCTCTGGCGGTGTCCCTGCAAGAACTGGTTCTGCCAGCCTGCTCAATTTTGGTCCCTG
CTGTTTTTGTATGAGCCTTTTGTCTGTTTCTCCTTCCACCCTGCTGGCTGGGCGGCTGCACTC
AGCATCACCCCTTCTGGGTGGCATGTCTCTCTCTACCTCATTTTTAGAACCAAGAACATC
TGAGATGATTCTCTACCCTCATCCACATCTAGCCAAGCCAGTGACCTTGCTCTGGTGGCACT
GTGGGAGACACCACTTGTCTTTAGGTGGGTCTCAAAGATGATGTAGAATTTCTTTAATTTT
TCGCAGTCTTCTGGAAAAATATTTTCTTTGAGCAGCAAATCTTGTAGGGATATCAGTGAAG
GTCTCTCCCTCCCTCCTCTCCTGTTTTTTTTTTTTTTTGGAGACAGAGTTTTGCTCTTGTGTC
CAGGCTGGAGTGTGATGGCTCGATCTTGGCTCACCACAACCTCTGCCTCCTGGGTTCAGCA
ATTCTCCTGCCTCAGCCTCTTGAGTAGCTTGGTTTATAGGCGCATGCCACCATGCCTGGCTA
ATTTTGTGTTTTTAGTAGAGACAGGGTTTCTCCATGTTGGTCAGGCTGGTCTCAAACCTCCA
ACCTCAGGTGATCTGCCCTCCTTGGCCTCCAGAGTGCTGGGATTACAGGTGTGAGCCACTG
TGCCGGGCCCCGTCCCCCTCCTTTTTTAGGCCTGAATACAAAGTAGAAGATCACTTTCCTTAC
TGTGCTGAGAATTTCTAGATACTACAGTTCTTACTCCTCTCTTCCCTTTGTTATTAGTGTG
ACCAGGATGGCGGGAGGGGATCTGTGTCACTGTAGGTACTGTGCCAGGAAGGCTGGGTGAA
GTGACCATCTAAATTCAGGATGGTGAAATTATCCCCATCTGTCTAATGGGCTTACCTCCT
CTTTGCCTTTTGAACCTCACTTCAAAGATCTAGGCCTCATCTTACAGGTCTTAAATCACTCAT
CTGGCCTGGATAATCTCACTGCCCTGGCACATTCCCATTGTGTGCTGTGGTGTATCCTGTGTT
TCCTTGTCTGGTTTGT
TCTGTCTATTTTGTATCCTGGACCACAAGTTCCTAAGTAGAGCAAGAATTCATCAACCAGCT
GCCTCTTGTTCATTTACCTCAGCACGTACCATCTGTCTTTTGTGTGTGTGTGTGTGTGTGT
TTGTTTTTTTGTCTTTTACCAAACATGTCTGTAAATCTTAACCTCCTGCCTAGGATTTGTACA
GCATCTGGTGTGTGCTTATAAGCCAATAAATATTCAATGTGAAAAAAAAAAAAAAAAA

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FIGURE 134

MRWILFIGALIGSSICGQEKFFGDQVLRINVRNGDEISKLSQLVNSNNLKLNFWKSPSSFNR
PVDVLVPSVSLQAFKSFLRSQGLEAYVTIEDLQALLDNEDDEMQHNEGQERSNNFNYGAYH
SLEAIYHEMDNIAADFPDLARRVKIGHSFENRPMYVLKFSTGKGVRRPAVWLNAGIHSREWI
SQATAIWTARKIVSDYQRDPAITSILEKMDIFLLPVANPDGYVYTQTQNRLWRKTRSRNPGS
SCIGADPNRNWNASFAGKGASDNPCSEVYHGPHANSEVEVKSVVDFIQKHGNFKGFIDLHSY
SQLLMYPYGYSVKKAPDAEELDKVARLAAKALASVSGTEYQVGPTCTTVYPASGSSIDWAYD
NGIKFAFTFELRDTGTYGFLLPANQIIPTAEETWLGLKTIMEHVRDONLY

Signal peptide:

amino acids 1-16

FIGURE 135

CAACCATGCAAGGACAGGGCAGGAGAAGAGGAACCTGCAAAGACATATTTTGTTCCAAAATG
GCATCTTACCTTTATGGAGTACTCTTTGCTGTTGGCCTCTGTGCTCCAATCTACTGTGTGTC
CCCGGCCAATGCCCCCAGTGCATACCCCCGCCCTTCCTCCACAAAGAGCACCCCTGCCTCAC
AGGTGTATTCCCTCAACACCGACTTTGCCTTCCGCCTATACCGCAGGCTGGTTTTGGAGACC
CCGAGTCAGAACATCTTCTTCTCCCCTGTGAGTGTCTCCACTTCCCTGGCCATGCTCTCCCT
TGGGGCCCACTCAGTCACCAAGACCCAGATTCTCCAGGGCCTGGGCTTCAACCTCACACACA
CACCAGAGTCTGCCATCCACCAGGGCTTCCAGCACCTGGTTCACTCACTGACTGTTCCAGC
AAAGACCTGACCTTGAAGATGGGAAGTGCCCTCTTCGTCAAGAAGGAGCTGCAGCTGCAGGC
AAATTTCTTGGGCAATGTCAAGAGGCTGTATGAAGCAGAAGTCTTTTCTACAGATTTCTCCA
ACCCCTCCATTGCCCAGGCGAGGATCAACAGCCATGTGAAAAAGAAGACCCAAGGGAAGGTT
GTAGACATAATCCAAGGCCTTGACCTTCTGACGGCCATGGTTCTGGTGAATCACATTTTCTT
TAAAGCCAAGTGGGAGAAGCCCTTTCACCTTGAATATACAAGAAAGAACTTCCCATTCCTGG
TGGGCGAGCAGGTCACTGTGCAAGTCCCCATGATGCACCAGAAAGAGCAGTTCGCTTTTGGG
GTGGATACAGAGCTGAACTGCTTTGTGCTGCAGATGGATTACAAGGGAGATGCCGTGGCCTT
CTTTGTCTCCTTAGCAAGGGCAAGATGAGGCAACTGGAACAGGCCTTGTGAGCCAGAACAC
TGATAAAGTGGAGCCACTCACTCCAGAAAAGGTGGATAGAGGTGTTTATCCCCAGATTTTCC
ATTTCTGCCTCCTACAATCTGGAAACCATCCTCCCGAAGATGGGCATCCAAAATGCCTTTGA
CAAAAATGCTGATTTTTTCTGGAATTGCAAAGAGAGACTCCCTGCAGGTTTCTAAAGCAACCC
ACAAGGCTGTGCTGGATGTCAGTGAAGAGGGCACTGAGGCCACAGCAGCTACCACCACCAAG
TTCATAGTCCGATCGAAGGATGGTCCCTCTTACTTCACTGTCTCCTTCAATAGGACCTTCCT
GATGATGATTACAAATAAAGCCACAGACGGTATTCTCTTTCTAGGGAAAGTGGAAAATCCCA
CTAAATCCTAGGTGGGAAATGGCCTGTAACTGATGGCACATTGCTAATGCACAAGAAATAA
CAAACCACATCCCTCTTTCTGTTCTGAGGGTGCATTTGACCCCAGTGGAGCTGGATTTCGCTG
GCAGGGATGCCACTTCCAAGGCTCAATCACCAAACCATCAACAGGGACCCAGTCACAAGCC
AACACCCATTAACCCCAAGTCAGTGCCCTTTTCCACAAATTCTCCAGGTAAGTACTGCTTCATG
GGATGTTGCTGGGTTACCATATTTCCATTCCCTGGGGCTCCCAGGAATGGAAATACGCCAAC
CCAGGTTAGGCACCTCTATTGCAGAATTACAATAACACATTCAATAAAACTAAAATATGAAT
TCAA
AAAAAA

FIGURE 136

MASYLYGVLFVAVGLCAPIYCVSPANAPSAYPRPSSTKSTPASQVYSLNTDFAFRLYRRLVLE
TPSQNIFFSPVSVSTSLAMLSLGAHSVTKTQILQGLGFNLTHTPESAIHQGFQHLVHSLTVP
SKDLTLKMGSALFVKKELQLQANFLGNVKRLYEAEVFSTDFSNPSIAQARINSHVKKKTQ GK
VVDIIQGLDLLTAMVLVNHIFFKAKWEKPFHLEYTRKNFPFLVGEQVTVQVPMHQKEQFAF
GVDTELNCFVLQMDYKGDVAFFVLPSKGKMRQLEQALSARTLIKWSHSLQKRWIEVFIPRF
SISASYNLETILPKMGIQNAFDKNADFSGIAKRDSLQVSKATHKAVLDVSEEGTEATAATTT
KFIVRSKDGPSYFTVSFNRTFLMMITNKATDGILFLGKVENPTKS

Signal peptide:

amino acids 1-20

137/270

FIGURE 137

GGCTGACCGTGCTACATTGCCTGGAGGAAGCCTAAGGAACCCAGGCATCCAGCTGCCCACGC
CTGAGTCCAAGATTCTTCCCAGGAACACAAACGTAGGAGACCCACGCTCCTGGAAGCACCAG
CCTTTATCTCTTCACCTTCAAGTCCCCTTTCTCAAGAATCCTCTGTTCTTTGCCCTCTAAAG
TCTTGGTACATCTAGGACCCAGGCATCTTGCTTTCCAGCCACAAAGAGACAGATGAAGATGC
AGAAAGGAAATGTTCTCCTTATGTTTGGTCTACTATTGCATTTAGAAGCTGCAACAAATTCC
AATGAGACTAGCACCTCTGCCAACACTGGATCCAGTGTGATCTCCAGTGGAGCCAGCACAGC
CACCAACTCTGGGTCCAGTGTGACCTCCAGTGGGGTCCAGCACAGCCACCATCTCAGGGTCCA
GCGTGACCTCCAATGGGGTCCAGCATAGTCACCAACTCTGAGTTCATACAACTCCAGTGGG
ATCAGCACAGCCACCAACTCTGAGTTCAGCACAGCGTCCAGTGGGATCAGCATAGCCACCAA
CTCTGAGTCCAGCACAACTCCAGTGGGGCCAGCACAGCCACCAACTCTGAGTCCAGCACAC
CCTCCAGTGGGGCCAGCACAGTCCCAACTCTGGGTCCAGTGTGACCTCCAGTGGAGCCAGC
ACTGCCACCAACTCTGAGTCCAGCACAGTGTCCAGTAGGGCCAGCACTGCCACCAACTCTGA
GTCTAGCACACTCTCCAGTGGGGCCAGCACAGCCACCAACTCTGACTCCAGCACAACTCCA
GTGGGGCTAGCACAGCCACCAACTCTGAGTCCAGCACAACTCCAGTGGGGCCAGCACAGCC
ACCAACTCTGAGTCCAGCACAGTGTCCAGTAGGGCCAGCACTGCCACCAACTCTGAGTCCAG
CACAACTCCAGTGGGGCCAGCACAGCCACCAACTCTGAGTCCAGAACGACCTCCAATGGGG
CTGGCACAGCCACCAACTCTGAGTCCAGCACGACCTCCAGTGGGGCCAGCACAGCCACCAAC
TCTGACTCCAGCACAGTGTCCAGTGGGGCCAGCACTGCCACCAACTCTGAGTCCAGCACGAC
CTCCAGTGGGGCCAGCACAGCCACCAACTCTGAGTCCAGCACGACCTCCAGTGGGGCTAGCA
CAGCCACCAACTCTGACTCCAGCACAACTCCAGTGGGGCCGGCACAGCCACCAACTCTGAG
TCCAGCACAGTGTCCAGTGGGATCAGCACAGTCCCAATTCTGAGTCCAGCACACCCTCCAG
TGGGGCCAACACAGCCACCAACTCTGAGTCCAGTACGACCTCCAGTGGGGCCAACACAGCCA
CCAACTCTGAGTCCAGCACAGTGTCCAGTGGGGCCAGCACTGCCACCAACTCTGAGTCCAGC
ACAACCTCCAGTGGGGTCCAGCACAGCCACCAACTCTGAGTCCAGCACAACTCCAGTGGGGC
TAGCACAGCCACCAACTCTGACTCCAGCACAACTCCAGTGGGGCCAGCACAGCCACCAACT
CTGAGTCTAGCACAGTGTCCAGTGGGATCAGCACAGTCCCAATTCTGAGTCCAGCACAACT
TCCAGTGGGGCCAACACAGCCACCAACTCTGGGTCCAGTGTGACCTCTGCAGGCTCTGGAAC
AGCAGCTCTGACTGGAATGCACACAACTTCCCATAGTGCATCTACTGCAGTGAAGGCAA
AGCCTGGTGGGTCCCTGGTGGCGTGGGAAATCTTCCTCATCACCTGGTCTCGGTTGTGGCG
GCCGTGGGGCTCTTTGCTGGGCTCTTCTTCTGTGTGAGAAACAGCCTGTCCCTGAGAAACAC
CTTTAACACAGCTGTCTACCACCCTCATGGCCTCAACCATGGCCTTGGTCCAGGCCCTGGAG
GGAATCATGGAGCCCCCACAGGCCAGGTGGAGTCTTAAGTGGTCTGGAGGAGACCAGTA
TCATCGATAGCCATGGAGATGAGCGGGAGGAACAGCGGGCCCTGAGCAGCCCCGGAAGCAAG
TGCCGCATTCTTCAGGAAGGAAGAGACCTGGGCACCCAAGACCTGGTTTCCTTTTCATTCATC
CCAGGAGACCCCTCCCAGCTTTGTTTGAGATCCTGAAAATCTTGAAGAAGGTATTCCTCACC
TTTCTTGCCCTTTACCAGACACTGGAAAGAGAATACTATATTGCTCATTTAGCTAAGAAATAA
ATACATCTCATCTAACACACACGACAAAGAGAAGCTGTGCTTGCCCCGGGGTGGGTATCTAG
CTCTGAGATGAACTCAGTTATAGGAGAAAACCTCCATGCTGGACTCCATCTGGCATTCAAAA
TCTCCACAGTAAAATCCAAAGACCTCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
AAAAAAAAAAAAAAAAAAAA

1381270

FIGURE 138

MKMQKGNVLLMFGLLLHLEAATNSNETSTSANTGSSVISSGASTATNSGSSVTSSGVSTATI
SGSSVTSNGVSIVTNSEFHTTSSGISTATNSEFSTASSGISIATNSESSTTSSGASTATNSE
SSTPSSGASTVTNSGSSVTSSGASTATNSESSTVSSRASTATNSESSTLSSGASTATNSDSS
TTSSGASTATNSESSTTSSGASTATNSESSTVSSRASTATNSESSTTSSGASTATNSESRTT
SNGAGTATNSESSTTSSGASTATNSDSSTVSSGASTATNSESSTTSSGASTATNSESSTTSS
GASTATNSDSSSTTSSGAGTATNSESSTVSSGISTVTNSESSTPSSGANTATNSESSTTSSGA
NTATNSESSTVSSGASTATNSESSTTSSGVSTATNSESSTTSSGASTATNSDSSSTSSEAST
ATNSESSTVSSGISTVTNSESSTTSSGANTATNSGSSVTSAGSGTAALTGMHTTSHSASTAV
SEAKPGGSLVPWEIFLITLVSVVAAVGLFAGLFFCVRNSLSLRNTFNTAVYHHPHGLNHGLGP
GPGGNHGAPHRPRWSPNWFWRPVS SIAMEMSGRNSGP

Signal peptide:

amino acids 1-20

Transmembrane domain:

amino acids 510-532

FIGURE 139

GGGAGAGAGGATAAATAGCAGCGTGGCTTCCCTGGCTCCTCTCTGCATCCTTCCCGACCTTC
CCAGCAATATGCATCTTGACGTCTGGTCGGCTCCTGCTCCCTCCTTCTGCTACTGGGGGCC
CTGTCTGGATGGGCGGCCAGCGATGACCCCATGAGAAGGTCATTGAAGGGATCAACCGAGG
GCTGAGCAATGCAGAGAGAGAGGTGGGCAAGGCCCTGGATGGCATCAACAGTGGAATCACGC
ATGCCCGAAGGGAAGTGGAGAAGGTTTTCAACGGACTTAGCAACATGGGGAGCCACACCGGC
AAGGAGTTGGACAAAGGCGTCCAGGGGCTCAACCACGGCATGGACAAGGTTGCCCATGAGAT
CAACCATGGTATTGGACAAGCAGGAAAGGAAGCAGAGAAGCTTGGCCATGGGGTCAACAACG
CTGCTGGACAGGCCGGGAAGGAAGCAGACAAAGCGGTCCAAGGGTTCACACTGGGGTCCAC
CAGGCTGGGAAGGAAGCAGAGAACTTGGCCAAGGGGTCAACCATGCTGCTGACCAGGCTGG
AAAGGAAGTGGAGAAGCTTGGCCAAGGTGCCCACCATGCTGCTGGCCAGGCCGGGAAGGAGC
TGCAGAATGCTCATAATGGGGTCAACCAAGCCAGCAAGGAGGCCAACCAGCTGCTGAATGGC
AACCATCAAAGCGGATCTTCCAGCCATCAAGGAGGGGCCACAACCACGCCGTTAGCCTCTGG
GGCCTCAGTCAACACGCCTTTCATCAACCTTCCCGCCCTGTGGAGGAGCGTCGCCAACATCA
TGCCCCTAAACTGGCATCCGGCCTTGCTGGGAGAATAATGTCGCCGTTGTACATCAGCTGAC
ATGACCTGGAGGGGTTGGGGGTGGGGGACAGGTTTCTGAAATCCCTGAAGGGGGTTGTACTG
GGATTTGTGAATAAACTTGATACACCA

,40/270

FIGURE 140

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA66675

><subunit 1 of 1, 247 aa, 1 stop

><MW: 25335, pI: 7.00, NX(S/T): 0

MHLARLVGSCSLLLLLLGALSGWAASDDPIEKVIEGINRGLSNAEREVGKALDGINSGITHAG
REVEKVFNGLSNMGSHTGKELDKGVQGLNHGMDKVAHEINHGIGQAGKEAEKLGHGVNNAAG
QAGKEADKAVQGFHTGVHQAGKEAEKLGQGVNHAADQAGKEVEKLGQGAHHAAGQAGKELQN
AHNGVNQASKEANQLLNGNHQSGSSSHQGGATTTPLASGASVNTPFINLPALWRSVANIMP

Important features of the protein:

Signal peptide:

amino acids 1-25

Homologous region to circumsporozoite (CS) repeats:

amino acids 35-225

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FIGURE 141

CTCCGGGTCCCCAGGGGCTGCGCCGGGCCGGCTGGCAAGGGGGACGAGTCAGTGGACACTCCAGGAAGAGCGGC
CCCCGGGGGGCGATGACCGTGCGCTGACCTGACTCACTCCAGGTCCGGAGGCGGGGCCCCCGGGCGACTCG
GGGGCGGACCGCGGGGCGGAGCTGCCGCCGTGAGTCCGGCCGAGCCACCTGAGCCCGAGCCGCGGGACACCGTC
GCTCCTGCTCTCCGAATGCTGCGCACCGCGATGGGCTGAGGAGCTGGCTCGCCGCCCATGGGCGCGCTGCCG
CCTCGGCCACCGTGCTGCTGCTCCTGCTGCTGCTGCTCCTGCTGCGAGCCGCCCTCCGACCTGGGCGCTCAGC
CCCCGGATCAGCCTGCCCTGCGGCTCTGAAGAGCGGCCATTCTCAGATTCTGAAGCTGAACACATCTCCAACCTAC
ACAGCCCTTCTGCTGAGCAGGGATGGCAGGACCTGTACGTGGGTGCTCGAGAGGCCCTCTTTGCACTCAGTAGC
AACCTCAGCTTCTGTCAGGCGGGGAGTACCAGGAGCTGCTTTGGGGTGAGACGCAGAGAAGAAACAGCAGTGC
AGCTTCAAGGGCAAGGACCCACAGCGCGACTGTCAAACTACATCAAGATCCTCCTGCCGCTCAGCGGCAGTCAC
CTGTTCACTTGTGGCACAGCAGCCTTCAGCCCCATGTGTACCTACATCAACATGGAGAATTCACCCTGGCAAGG
GACGAGAAGGGGAATGTCTCCTGGAAGATGGCAAGGGCCGTGTGCCCTTCGACCCGAATTTCAAGTCCACTGCC
CTGGTGGTTGATGGCGAGCTCTACACTGGAACAGTCAGCAGCTTCCAAGGGAATGACCCGGCCATCTCGCGGAGC
CAAAGCCTTCGCCCCACCAAGACCGAGAGCTCCCTCAACTGGCTGCAAGACCCAGCTTTTGTGGCCTCAGCCTAC
ATTCTGAGAGCCTGGGCGCTTGAAGGCGATGATGACAAGATCTACTTTTTCTTCAGCGAGACTGGCCAGGAA
TTTGAGTTCTTTGAGAACACCATTGTGTCCCGCATTGCCCGCATCTGCAAGGGCGATGAGGGTGGAGAGCGGGTG
CTACAGCAGCGCTGGACCTCCTTCTCAAGGCCAGCTGCTGTGCTCACGGCCGACGATGGCTTCCCTTCAAC
GTGCTGCAGGATGTCTTACGCTGAGCCCCAGCCCCAGGACTGGCGTGACACCCTTTTCTATGGGTCTTCACT
TCCCAGTGGCACAGGGGAATACAGAAGGCTCTGCCGTCTGTGTCTTACAATGAAGGATGTGAGAGAGTCTTC
AGCGGCCTCTACAAGGAGGTGAACCGTGAGACACAGCAGTGGTACACCGTGACCCACCCGGTGCCACACCCCGG
CCTGGAGCGTGATCACCAACAGTGCCCGGGAAGGAAGATCAACTCATCCCTGCAGCTCCAGACCGCGTGCTG
AACTTCTCAAGGACCACTTCTGATGGACGGGCGAGGTCCGAAGCCGCATGCTGCTGTCAGCCCCAGGCTCGC
TACCAGCGCGTGGCTGTACACCGCTCCTTGGCCTGCACCACACCTACGATGTCTCTTCTTGGGCACTGGTGAC
GGCCGGCTCCACAAGGCAGTGAGCGTGGGCCCCGGGTGCACATCATTGAGGAGCTGCAGATCTTCTCATCGGGA
CAGCCCGTGCGAATCTGCTCCTGGACACCCACAGGGGGCTGCTGTATGCGGCCTCACACTCGGGCGTAGTCCAG
GTGCCCATGGCCAATGCGAGCCTGTACCGGAGCTGTGGGACTGCCTCCTCGCCCGGGACCCCTACTGTGCTTG
AGCGGCTCCAGCTGCAAGCACGTACGCTTACAGCCTCAGCTGGCCACCAGGCGGTGGATCCAGGACATCGAG
GGAGCCAGCGCCAAGGACCTTTGCGAGCGCTCTCGGTTGTGTCCCGCTCTTTGTACCAACAGGGGAGAAGCCA
TGTGAGCAAGTCCAGTTCCAGCCCAACACAGTGAACACTTTGGCCTGCCCGCTCCTCTCCAACCTGGCGACCCGA
CTCTGGCTACGCAACGGGGCCCCCGTCAATGCCCTCGGCCCTGCCACGTGCTACCCACTGGGGACCTGCTGCTG
GTGGGCACCCAACAGCTGGGGGAGTTCCAGTGTGCTGCTACTAGAGGAGGGCTTCCAGCAGCTGGTAGCCAGCTAC
TGCCAGAGGTGGTGGAGGACGGGGTGGCAGACCAACAGATGAGGGTGGCAGTGTACCCGTCATTATCAGCACA
TCGCGTGTGAGTGACACAGCTGGTGGCAAGGCCAGCTGGGGTGAGACAGGTCTTACTGGAAGGAGTTCTGGTG
ATGTGCACGCTCTTTGTGCTGGCCGTGCTGCTCCAGTTTATTCTTGTCTTACCGGCACCGGAACAGCATGAAA
GTCTTCTGAAGCAGGGGAATGTGCCAGCGTGACCCCAAGACCTGCCCTGTGGTGTGCTGCCCTGAGACCCGC
CCACTCAACGGCCTAGGGCCCCCTAGCACCCCGCTCGATCACCGAGGGTACCAGTCCCTGTGAGACAGCCCCCG
GGGGCCCGAGTCTTCACTGAGTCAGAGAAGAGGCCACTCAGCATCCAAGACAGCTTCGTGGAGGTATCCCCAGTG
TGCCCCCGGCCCGGGTCCGCCCTTGGCTCGGAGATCCGTGACTCTGTGGTGTGAGAGCTGACTTCCAGAGGACGC
TGCCCTGGCTTACGGGGCTGTGAATGCTCGGAGAGGGTCAACTGGACCTCCCTCCGCTCTGCTCTTCTGTGAAC
ACGACCGTGGTGCCCGGCCCTTGGGAGCCTTGGAGCCAGCTGGCCTGCTGCTCTCCAGTCAAGTAGCGAAGCTCC
TACCACCCAGACACCAACAGCCGTGGCCCCAGAGGTCTTGCCCAAATATGGGGGCTGCCTAGGTTGGTGGAA
CAGTGCTCCTTATGTAACTGAGCCCTTTGTTTAAAAACAATTCCAATGTGAACTAGAAATGAGAGGGAAGAG
ATAGCATGGCATGCAGCACACAGGCTGCTCCAGTTTCATGGCCTCCAGGGGTGCTGGGGATGCATCCAAAGTGG
TTGTCTGAGACAGAGTTGGAACCCCTACCAACTGGCCTCTTACCTTCCACATTATCCCGCTGCCACCGGCTGC
CCTGTCTCACTGCAGATTACAGACAGCTTGGGCTGCGTGCGTTCTGCTTGGCAGTCAGCCGAGGATGTAGTTG
TTGCTCGCGTCTGCTCCACCACTCAGGACAGCTTGGGCTGCGTGCGTTCTGCTTGGCAGTCAGCCGAGGATGTAGTTG
GGACCAACTCCTGGACCTTCCAGCCTGTATCAGGCTGTGGCCACACGAGAGGACGAGGCTCAGGAGAGA
TTTCTGTGACAATGTACGCCTTTCCCTCAGAATTCAAGGAAGAGACTGTGCGCTGCCTTCTCCGTTGTTGCGTGA
GAACCCGTGTGCCCCCTTCCACCATATCCACCCTCGCTCCATCTTTGAACTCAAACACGAGGAACCTAAGTGCACC
CTGGTCTCTCCCCAGTCCCCAGTTACCCCTCCATCCCTCACCTTCTTCACTCTAAGGGATATCAACACTGCCC
AGCACAGGGGCCCTGAATTTATGTGGTTTTTATACATTTTTTAATAAGATGCACCTTATGTCAATTTTTTAATAAA
GTCTGAAGAATTACTGTTTAAAAA

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FIGURE 142

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA67962

><subunit 1 of 1, 837 aa, 1 stop

><MW: 92750, pI: 7.04, NX(S/T): 6

MLRTAMGLRSWLAAPWGALPPRPPLLLLLLLLLLLLLLQPPPPTWALSPRISLPLGSEERPFLRF
EAEHISNYTALLLSRDGRTLTVGAREALFALSSNLSFLPGGEYQELLWGADAEKKQQCSFKG
KDPQRDCQNYIKILLPLSGSHLFTCGTAAAFSPMCTYINMENFTLARDEKGNVLLEDGKGRCP
FDPNFKSTALVVDGELYTGTVSSFQGNPAISRSQSLRPTKTESSLNWLQDPAFVASAYIPE
SLGSLQGDDDKIYFFFSETGQEFEFFENTIVSRIARICKGDEGGERVLQQRWTSFLKAQLLC
SRPDDGFPFNVLQDVFTLSPSPQDWRDTLFYGVFTSQWHRGTTEGSAVCVFTMKDVQRVFSG
LYKEVNRETQQWYTVTHPVPTPRPGACITNSARERKINSSLQLPDRVLNFKDHFLLMDGQVR
SRMLLLQPQARYQRVAVHRVPGLHHTYDVLFLGTGDGRLHKAVSVGPRVHIIEELQIFSSGQ
PVQNLLLDTHRGLLYAASHSGVVQVPMANCSLYRSCGDCLLARDPYCAWSGSSCKHVSLEYQP
QLATRPWIQDIEGASAKDLCSASSVVSPSFVPTGEKPCQVQFQPNVTNLTACPLLSNLATR
LWLRNGAPVNASASCHVLPTGDLLLVTGQQLGFEFQCWSLEEGFQQLVASYCPEVVEDGVADQ
TDEGGSVPVIIISTSRVSAPAGGKASWGADRSYWKEFLVMCTLFVLAVLLPVLFLLYRHRNSM
KVFLKQGECAVHPKTCPVVLPETRPLNGLGPPSTPLDHRGYQSLSDSPPGARVFTSESEKR
PLSIQDSFVEVSPVCPRPRVRLGSEIRDSVV

Transmembrane domains:

amino acids 23-46 (type II), 718-738

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FIGURE 143A

CTAAGCCGGAGGATGTGCAGCTGCGGCGGCGGCGCGGCTACGAAGAGGACGGGGACAGGCGCCGTGCGAACC
GCCCCAGCCAGCCGGAGGACGCGGGCAGGGCGGGACGGGAGCCCGACTCGTCTGCCGCCGCCGTGTCGCCGT
TGCCGGCCCCCGCTCCCCGCGCGGAGCGGGAGGAGCCGCCGCCACCTCGCGCCCCGAGCCGCCGCTAGCGCGCGC
CGGGCATGGTCCCCTCTTAAAGGCGCAGGCCGCGGCGGGGGCGGGTGTGCGGAACAAAGCGCGGCGCGGGG
CCTGCGGGCGGCTCGGGGGCGCGATGGGCGCGGCGGGGCCGCGGCGGGCGGCGCTGCCCGGGCCGGGCTCG
CGGCGCTAGGGCGGGCTGGCCTCCGTGGGCGGGGCGAGCGGGCTGAGGGCGCGCGGAGCCTGCGGCGGCGGGC
GGCGGCGGCGGCGGCCCGGCGGGCGGAGCGGCGCGGGCATGCGCGCGCGGCGCGGCGGCGGCTGGCTCAGCGTGC
TGCTCGGGCTCGTCTGGGCTTCGTGCTGGCCTCGCGGCTCGTCTGCCCGGGCTTCCGAGCTGAAGCGAGCGG
GCCACGGCGCGCGCCAGCCCCGAGGGCTGCCGGTCCGGGCGAGGCGGCGGCTTCCAGGCCGGCGGGGCGCGCG
GCGATGCGCGCGGGGCGCAGCTCTGGCCGCCCGGCTCGGACCCAGATGGCGGCCCGCGCGACAGGAACCTTCTCT
TCGTGGGAGTCATGACCGCCCAGAAATACCTGCAGACTCGGGCCGTGGCCGCTACAGAACATGGTCCAAGACAA
TTCTTGGGAAAGTTTCACTTCTTCTCAAGTGAGGGTTCTGACACATCTGTACCAATTCAGTAGTGCCACTACGGG
GTGTGGACGACTCTTACCCGCCCGAGAAGAAGTCTTTCATGATGCTCAAGTACATGCACGACCACTACTTGGACA
AGTATGAATGGTTTATGAGAGCAGATGATGACGTGACATCAAAGGAGACCGTCTGGAGAATCTTCTGAGGAGTT
TGACAGCAGCGAGCCCCCTCTTCTTGGGCGAGCAGGCTGGGACCACGGAAGAAATGGGAAAATGGCCCTGG
AGCCTGGTGAGAACTTCTGCATGGGGGGGCTGGCGTGATCATGAGCCGGGAGGTGCTTCGGAGAATGGTGCCGC
ACATTGGCAAGTGTCTCCGGGAGATGTACACCACCCATGAGGACGTGGAGGTGGGAAGGTGTGTCCGGAGGTTTG
CAGGGGTGCAGTGTGTCTGGTCTTATGAGATGCGGCAGCTTTTTTATGAGAATTACGAGCAGAACAAAAGGGGT
ACATTAGAGATCTCCATAACAGTAAATTCACCAAGCTATCACATTACCCCCAACAAAACCCACCCTACCAGT
ACAGGCTCCACAGCTACATGCTGAGCCGCAAGATATCCGAGCTCCGCCATCGCACAATACAGCTGCACCGCGAAA
TTGTCCTGATGAGCAAATACAGCAACACAGAAATTCATAAAGAGGACCTCCAGCTGGGAATCCCTCCCTCCTTCA
TGAGGTTTCAGCCCCGCCAGCGAGAGGAGATTCTGGAATGGGAGTTTCTGACTGGAAAATACTTGTATTCCGCAG
TTGACGGCCAGCCCCCTCGAAGAGGAATGGACTCCGCCCGAGAGGGAAGCCTTGGACGACATTGTCTATGCAGGTCA
TGGAGATGATCAATGCCAACGCCAAGACCAGAGGGCGCATATTGACTTCAAAGAGATCCAGTACGGCTACCGCC
GGGTGAACCCCATGTATGGGGCTGAGTACATCCTGGACCTGCTGCTTCTGTACAAAAGCACAAGGGAAGAAAA
GACCGTCCCTGTGAGGAGGCACGCTATTTACAGCAGACTTTCAGCAAAATCCAGTTTGTGAGCAGTAGGAGC
TGGATGCACAAGAGTTGGCCAAGAGAATCAATCAGGAATCTGGATCCTTGTCTTCTCAAACCTCCCTGAAGA
AGCTCGTCCCCCTTTCAGCTCCCTGGGTGCAAGAGTGAGCACAAGAACCACAAAGATAAAAAAGATAAACATACTGA
TTCTTTTGTCTGGGCGTTTCGACATGTTTGTGAGATTTATGGGAACTTTGAGAAGACGTGTCTTATCCCCAATC
AGAACGTCAAGCTCGTGGTTCTGCTTTTCAATTCTGACTCCAACCCTGACAAGGCCAAACAAGTTGAAGTATGA
GAGATTACCGCATTAAGTACCCTAAAGCCGACATGCAGATTTTGCCTGTGTCTGGAGAGTTTCAAGAGCCCTGG
CCCTGGAAGTAGGATCCTCCAGTTTAAACAATGAATCTTTGCTCTTCTTCTCGACGTGACCTCGTGTTTACTA
CAGAATTCCTTCAGCGATGTGAGCAAATACAGTTCTGGGCCAACAAATATATTTTCCAATCATCTTCAGCCAGT
ATGACCCAAAGATTGTTTATAGTGGGAAAGTTCCCAAGTGACAACCATTTTGCCTTTACTCAGAAAACCTGGCTTCT
GGAGAACTATGGGTTTGGCATCACGTGTATTTATAAGGGAGATCTTGTCCGAGTGGGTGGCTTTGATGTTTCCA
TCCAAGGCTGGGGCTGGAGGATGTGGACCTTTTCAACAAGGTTGTCCAGGCAGGTTTGAAGACGTTTAGGAGCC
AGGAAGTAGGATAGTCCACGTCCACCATCTGCTTTTGTGATCCCAATCTTGACCCCAACAGTACAAAATGT
GCTTGGGGTCCAAAGCATCGACCTATGGGTCCACCCAGCAGCTGGCTGAGATGTGGCTGGAAAAGATGATCCAA
GTTACAGTAAAAGCAGCAATAATAATGGCTCAGTGAGGACAGCCTAAATGTCCAGCTTTTGTGAAAAGACGTTTT
TAATTATCTAATTTATTTTTCAAAAATTTTTTGTATGATCAGTTTTTGAAGTCCGTATACAAGGATATATTTTAC
AAGTGGTTTTTCTTACATAGGACTCCTTTAAGATTGAGCTTTCTGAACAAGAAGGTGATCAGTGTGTGCTTTGAA
CACATCTTCTGTGAACATTATGTAGCAGACCTGCTTAACTTTGACTTGAATGTACCTGATGAACAAAACCTTT
TTTAAAAAATGTTTTCTTTTGGAGACCTTTGCTCCAGTCTTATGGCAGAAAACGTGAACATTCCTGCAAAGTAT
TATTGTAACAAAACACTGTAACCTCTGGTAAATGTTCTGTTGTGATTGTTAACATTCCACAGATTCTACCTTTTGT
GTTTTGTTTTTTTTTTTACAATTGTTTTAAAGCCATTTTCATGTTCCAGTTGTAAGATAAGGAAATGTGATAATA
GCTGTTTCATCATTGTCTTCAGGAGAGCTTTCCAGAGTTGATCATTTCCTCTCATGGTACTCTGCTCAGCATGGC
CACGTAGGTTTTTTGTTTGTGTTTTGTTTCTTTTTTGGAGACGGAGTCTCACTCTGTTACCCAGGCTGGAATG
CAGTGGCGCAATCTTGGCTCACTTTAACCTCCACTCCCTGGTTCAAGCAATTCCTTGCCTTGGCTCCCGAGT
AGCTGGGATTACAGGCACACACCACCGCCAGNTAGTTTTTTGTATTTTGTAGTAGAGACGGGGTTTACCAT
GCAAGCCCAGCTGGCCACGTAGGTTTTAAAGCAAGGGCGGTGAAGAAGGCACAGTGAGGTATGTGGCTGTTCTCG
TGGTAGTTTCATTTCGGCCTAAATAGACCTGGCATTAAATTTCAAGAAGGATTGGCATTCTCTCTTCTGACCTT
CTCTTTAAAGGGTAAATATTAATGTTTAGAATGACAAAGATGAATTATTACAATAAATCTGATGTACACAGACT
GAAACATACACACATACACCCTAATCAAAACGTTGGGGAAAAATGTATTTGGTTTTGTTCTTTTCATCCTGTCTG
TGTTATGTGGGTGGAGATGGTTTTTCACTCTTTCACTACTGTTTTGTTTTATCCTTTGTATCTGAAATACCTTTAA
TTTATTTAATATCTGTGTTTTCAGAGCTCTGCCATTTCTTGAGTACCTGTTAGTTAGTATTATTTATGTGTATCGG
GAGTGTGTTTAGTCTGTTTTATTTGCAGTAAACCGATCTCCAAAGATTTCTTTTGGAAACGCTTTTTTCCCTCC

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FIGURE 143B

TTAATTTTATATTCCTTACTGTTTTACTAAATATTAAGTGTTCTTTGACAATTTTGGTGCTCATGTGTTTTGGG
GACAAAAGTGAAATGAATCTGTCAATTATACCAGAAAGTTAAATTCTCAGATCAAATGTGCCCTTAATAAATTTGTT
TTCATTTAGATTTCAAACAGTGATAGACTTGCCATTTTAATACACGTCATTGGAGGGCTGCGTATTGTAAATAG
CCTGATGCTCATTTGGAAAAATAAACAGTGAACAATATTTTCTATTGTACTTTTGAACCATTTTGTCTCATT
ATTCCTGTTTTAGCTGAAGAATTGTATTACATTTGGAGAGTAAAAAATTAAACACGAAAAA

FIGURE 144

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68836

><subunit 1 of 1, 802 aa, 1 stop

><MW: 91812, pI: 9.52, NX(S/T): 3

MAARGRRAWLSVLLGLVLGFVLASRLVLPRASELKRAGPRRRASPEGCRSGQAAASQAGGAR
GDARGAQLWPPGSDPDGGPRDRNFLVGVMTAQKYLQTRAVAAYRTWSKTIPGKVQFFSSEG
SDTSVPIPVVPLRGVDDSYPPQKKSFMMMLKYMHDHYLDKYEWFMRADDDVYIKGDRLENFLR
SLNSSEPLFLGQTGLGTTEEMGKLALÉPGENFCMGGPGVIMSREVLRRMVPHIGHKCLREMYT
THEDVEVGRCVRRFAGVQCVWSYEMRQLFYENYEQNKKGYIRDLHNSKIHQAITLHPNKNPP
YQYRLHSYMLSRKISELRHRTIQLHREIVLMSKYSNTEIHKEDLQLGIPPSFMRFPQRQREE
ILEWEFLTGKYLYSAVDGQPPRRGMDSAQREALDDIVMQVMEMINANAKTRGRIIDFKEIQY
GYRRVNP MYGAEYILDLLLLYKKHKGKMTVPVRRHAYLQQTFSKIQFVEHEELDAQELAKR
INQESGSLSFLSNSLKKLVFPQLPGSKSEHKEPKDKKINILIPLSGRFDMFVRFMGNFEKTC
LIPNQNVKLVLVLLFNSDSNPDKAKQVELMRDYRIKYPKADMQILPVSGEFSRALALEVGSSQ
FNNESLLFFCDVDLVFTTEFLQRCRANTVLGQQIYFPIIFSQYDPKIVYSGKVPSDNHFAFT
OKTGFWRNYGFGITCIYKGD LVRVGGFDVSIQGWGLEDVDLFNKVVQAGLKTFRSQEVGVVH
VHHPVFCDPNLDPKQYKMCLGSKASTYGSTQQLAEMWLEKNDPSYSKSSNNNGSVRTA

Signal peptide:

amino acids 1-23

146/270

FIGURE 145

GGACAACCGTTGCTGGGTGTCCCAGGGCCTGAGGCAGGACGGTACTCCGCTGACACCTTCCC
TTTCGGCCTTGAGGTTCCAGCCTGGTGGCCCCAGGACGTTCCGGTCGCATGGCAGAGTGCT
ACGGACGACGCCTATGAAGCCCTTAGTCCTTCTAGTTGCGCTTTTGCTATGGCCTTCGTCTG
TGCCGGCTTATCCGAGCATAACTGTGACACCTGATGAAGAGCAAACTTGAATCATTATATA
CAAGTTTTAGAGAACCTAGTACGAAGTGTTCCCTCTGGGGAGCCAGGTCGTGAGAAAAAATC
TAACTCTCCAAAACATGTTTATTCTATAGCATCAAAGGGATCAAAATTTAAGGAGCTAGTTA
CACATGGAGACGCTTCAACTGAGAATGATGTTTTAACCAATCCTATCAGTGAAGAACTACA
ACTTTCCCTACAGGAGGCTTCAACCCGAAATAGGAAAGAAAAAACACACGGAAAGTACCCC
ATTCTGGTCGATCAAACCAAACAATGTTTCCATTGTTTTGCATGCAGAGGAACCTTATATTG
AAAATGAAGAGCCAGAGCCAGAGCCGGAGCCAGCTGCAAAACAACTGAGGCACCAAGAATG
TTGCCAGTTGTTACTGAATCATCTACAAGTCCATATGTTACCTCATACAAGTCACCTGTAC
CACTTTAGATAAGAGCACTGGCATTGAGATCTCTACAGAATCAGAAGATGTTCCCTCAGCTCT
CAGGTGAACTGCGATAGAAAAACCCGAAGAGTTTGAAAGCACCCAGAGAGTTGGAATAAT
GATGACATTTTGAAAAAAATTTTAGATATTAATTCACAAGTGCAACAGGCACTTCTTAGTGA
CACCAGCAACCCAGCATATAGAGAAGATATTGAAGCCTCTAAAGATCACCTAAAACGAAGCC
TTGCTCTAGCAGCAGCAGCAGAACATAAATTAAAAACAATGTATAAGTCCCAGTTATTGCCA
GTAGGACGAACAAGTAATAAAATTGATGACATCGAACTGTTATTAACATGCTGTGTAATTC
TAGATCTAACTCTATGAATATTTAGATATTAATGTGTTCCACCAGAGATGAGAGAAAAAG
CTGCTACAGTATTCAATACATTAAAAAATATGTGTAGATCAAGGAGAGTCACAGCCTTATTA
AAAGTTTATTAAACAATAATATAAAAAATTTTAAACCTACTTGATATTCATAACAAAGCTGA
TTTAAGCAAACCTGCATTTTTTTCACAGGAGAAATAATCATATTCGTAATTTCAAAGTTGTAT
AAAAATATTTTCTATTGTAGTTCAAATGTGCCAACATCTTTATGTGTCATGTGTTATGAACA
ATTTTCATATGCACTAAAAACCTAATTTAAAATAAAATTTTGTTTCAGGAAAAAA

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FIGURE 146

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68864

><subunit 1 of 1, 350 aa, 1 stop

><MW: 39003, pI: 5.59, NX(S/T): 1

MKPLVLLVALLLWPSSVPAYPSITVTPDEEQNLNHYIQVLENLVRSVPSGEPGREKKSNSPK
HVYSIASKGSKFKELVTHGDASTENDVLTNPISEETTTFTPTGGFTPEIGKKKHTSTPFWSI
KPNNVSIVLHAEOPYIENEEPEPEPEPAAKQTEAPRMLPVVTESSTSPYVTSYKSPVTTLDK
STGIEISTESEDVPQLSGETAIEKPPEEFGKHPESWNNDDILKKILDINSQVQQALLSDTSNP
AYREDIEASKDHLKRSLALAAAAEHKLKTMYSQLLPVGRTSNKIDDIETVINMLCNSRSKL
YEYLDIKCVPPEMREKAATVFNTLKNMCRSRRVTALLKVY

Signal peptide:

amino acids 1-19

FIGURE 147

CGGCTCGAGCGGCTCGAGTGAAGAGCCTCTCCACGGCTCCTGCGCCTGAGACAGCTGGCCTG
ACCTCCAAATCATCCATCCACCCCTGCTGTCTGTTTTCATAGTGTGAGATCAACCCACA
GGAATATCCATGGCTTTTGTGCTCATTTTGGTTCTCAGTTTCTACGAGCTGGTGTGAGGACA
GTGGCAAGTCACTGGACCGGGCAAGTTTGTCCAGGCCTTGGTGGGGGAGGACGCCGTGTTCT
CCTGCTCCCTCTTTCTGAGACCAGTGCAGAGGCTATGGAAGTGCGGTTCTTCAGGAATCAG
TTCCATGCTGTGGTCCACCTCTACAGAGATGGGGAAGACTGGGAATCTAAGCAGATGCCACA
GTATCGAGGGGAGAACTGAGTTTGTGAAGGACTCCATTGCAGGGGGGCGTGTCTCTCTAAGGC
TAAAAAACATCACTCCCTCGGACATCGGCCTGTATGGGTGCTGGTTTCAGTTCCAGATTTC
GATGAGGAGGCCACCTGGGAGCTGCGGGTGGCAGCACTGGGCTCACTTCCTCTCATTTCCAT
CGTGGGATATGTTGACGGAGGTATCCAGTTACTCTGCCTGTCTCAGGCTGGTTCCCCCAGC
CCACAGCCAAGTGGAAGGTCCACAAGGACAGGATTTGTCTTCAGACTCCAGAGCAAATGCA
GATGGGTACAGCCTGTATGATGTGGAGATCTCCATTATAGTCCAGGAAAATGCTGGGAGCAT
ATTGTGTTCCATCCACCTTGCTGAGCAGAGTCATGAGGTGGAATCCAAGTATTGATAGGAG
AGACGTTTTTCCAGCCCTCACCTTGGCGCCTGGCTTCTATTTTACTCGGGTTACTCTGTGGT
GCCCTGTGTGGTGTGTGTCATGGGGATGATAATTGTTTTCTTCAAATCCAAAGGGAAAATCCA
GGCGGAACTGGACTGGAGAAGAAAGCACGGACAGGCAGAATTGAGAGACGCCCGGAAACACG
CAGTGGAGGTGACTCTGGATCCAGAGACGGCTCACCCGAAGCTCTGCGTTTCTGATCTGAAA
ACTGTAACCCATAGAAAAGCTCCCCAGGAGGTGCCTCACTCTGAGAAGAGATTTACAAGGAA
GAGTGTGGTGGCTTCTCAGGGTTTCCAAGCAGGGAGACATTACTGGGAGGTGGACGTGGGAC
AAAATGTAGGGTGGTATGTGGGAGTGTGTCGGGATGACGTAGACAGGGGGAAGAACAATGTG
ACTTTGTCTCCCAACAATGGGTATTGGGTCTCAGACTGACAACAGAACATTTGTATTTTAC
ATTCAATCCCCATTTTATCAGCCTCCCCCCCAGCACCCCTCCTACACGAGTAGGGGTCTTCC
TGGACTATGAGGGTGGGACCATCTCCTTCTTCAATACAAATGACCAGTCCCTTATTTATACC
CTGCTGACATGTGAGTTTGAAGGCTTGTTGAGACCCTATATCCAGCATGCGATGTATGACGA
GGAAAAGGGGACTCCCATATTATATGTCCAGTGTCTTGGGGATTGAGACAGAGAAGACCTG
CTTAAAGGGCCCCACACCACAGACCCAGACACAGCCAAGGGAGAGTGCTCCCGACAGGTGGC
CCCAGCTTCTCTCCGGAGCCTGCGCACAGAGAGTCACGCCCCCACTCTCCTTTAGGGAGC
TGAGGTTCTTCTGCCCTGAGCCCTGCAGCAGCGGCAGTCACAGCTTCCAGATGAGGGGGGAT
TGGCCTGACCCTGTGGGAGTCAGAAGCCATGGCTGCCCTGAAGTGGGGACGGAATAGACTCA
CATTAGGTTTAGTTTGTGAAAACCTCCATCCAGCTAAGCGATCTTGAACAAGTCACAACCTCC
CAGGCTCCTCATTTGCTAGTCACGGACAGTGATTCTGCCTCACAGGTGAAGATTAAAGAGA
CAACGAATGTGAATCATGCTTGCAGGTTTGAGGGGCACAGTGTTTGCTAATGATGTGTTTTTA
TATTATACATTTTCCCACCATAAACTCTGTTTGCTTATTTCCACATTAAATTTACTTTTCTCTA
TACCAAATCACCCATGGAATAGTTATTGAACACCTGCTTTGTGAGGCTCAAAGAATAAAGAG
GAGGTAGGATTTTTTCACTGATTCTATAAGCCCAGCATTACCTGATACCAAACAGGCAAAG
AAAACAGAAGAAGAGGAAGGAAAACCTACAGGTCCATATCCCTCATTAAACACAGACACAAAA
TTCTAAATAAAATTTTAACAAATTAACCTAAACAATATTTTAAAGATGATATATACTACT
CAGTGTGGTTTGTCCCACAAATGCAGAGTTGGTTTAATATTTAAATATCAACCAGTGTAATT
CAGCACATTAATAAAGTAAAAAAGAAAACCATAAAAAAAAAAAAAAA

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FIGURE 148

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68866

><subunit 1 of 1, 466 aa, 1 stop

><MW: 52279, pI: 6.16, NX(S/T): 2

MAFVLILVLSFYELVSGQWQVTGPGKFVQALVGEDAVFSCSLFPETSAEAMEVRFFRNQFHA
VVHLYRDGEDWESKQMPQYRGRTEFVKDSIAGGRVSLRLKNITPSDIGLYGCWFSSQIYDEE
ATWELRVAALGSLPLISIVGYVDGGIQLLCLSSGWFPQPTAKWKGPQGQDLSSDSRANADGY
SLYDVEISIIVQENAGSILCSIHLAEQSHEVESKVLIGETFFQPSPWRLASILLGLLCGALC
GVVMGMIIVFFKSKGKIQAELDWRKKGQAELRDARKHAVEVTLPETAHPKLCVSDLKTVT
HRKAPQEVPHSEKRFRTRKSVVASQGFQAGRHYWEVDVGQNVGWYVGVCRDDVDRGKNNVTLS
PNNGYWVLRLTTEHLYFTFNPHFISLPPSTPPTRVGVFLDYEGGTISFFNTNDQSLIYTLT
CQFEGLLRPYIQHAMYDEEKGTPIFICPVSWG

Signal peptide:

amino acids 1-17

Transmembrane domains:

amino acids 131-150, 235-259

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FIGURE 149

CCTTCACAGGACTCTTCATTGCTGGTTGGCAATGATGTATCGGCCAGATGTGGTGAGGGCTA
GGAAAGAGTTTGTGGGAACCTGGGTTATCGGCCTCGTCATCTTCATATCCCTGATTGTC
CTGGCAGTGTGCATTGGACTCACTGTTTATTATGTGAGATATAATCAAAAGAAGACCTACAA
TTACTATAGCACATTGTCAATTTACAACTGACAACTATATGCTGAGTTTGGCAGAGAGGCTT
CTAACAATTTTACAGAAATGAGCCAGAGACTTGAATCAATGGTGAAAAATGCATTTTATAAA
TCTCCATTAAGGGAAGAATTTGTCAAGTCTCAGGTTATCAAGTTCAGTCAACAGAAGCATGG
AGTGTGGCTCATATGCTGTTGATTTGTAGATTTCACTCTACTGAGGATCCTGAACTGTAG
ATAAAATTGTTCAACTTGTTTTACATGAAAAGCTGCAAGATGCTGTAGGACCCCTAAAGTA
GATCCTCACTCAGTTAAAATTAAAAAATCAACAAGACAGAAACAGACAGCTATCTAAACCA
TTGCTGCGGAACACGAAGAAGTAAAACTCTAGGTGAGAGTCTCAGGATCGTTGGTGGGACAG
AAGTAGAAGAGGGTGAATGGCCCTGGCAGGCTAGCCTGCAGTGGGATGGGAGTCATCGCTGT
GGAGCAACCTTAATTAATGCCACATGGCTTGTGAGTGCTGCTCACTGTTTACACATATAA
GAACCTGCCAGATGGACTGCTTCCTTGGAGTAACAATAAAACCTTCGAAAATGAAACGGG
GTCTCCGGAGAATAATTGTCCATGAAAAATACAAACACCCATCACATGACTATGATATTTCT
CTTGACAGAGCTTTCTAGCCCTGTTCCCTACACAAATGCAGTACATAGAGTTTGTCTCCCTGA
TGCATCCTATGAGTTTCAACCAGGTGATGTGATGTTTGTGACAGGATTTGGAGCACTGAAAA
ATGATGGTTACAGTCAAAATCATCTTCGACAAGCACAGGTGACTCTCATAGACGCTACAACCT
TGCAATGAACCTCAAGCTTACAATGACGCCATAACTCCTAGAATGTTATGTGCTGGCTCCTT
AGAAGGAAAAACAGATGCATGCCAGGGTGAAGTCTGGAGGACCACTGGTTAGTTCAGATGCTA
GAGATATCTGGTACCTTGCTGGAATAGTGAGCTGGGGAGATGAATGTGCGAAACCCAACAAG
CCTGGTGTTTATACTAGAGTTACGGCCTTGCGGGACTGGATTACTTCAAAAACCTGGTATCTA
AGAGACAAAAGCCTCATGGAACAGATAACATTTTTTTTTTGTTTTTTGGGTGTGGAGGCCATT
TTTAGAGATACAGAATTGGAGAAGACTTGCAAAACAGCTAGATTTGACTGATCTCAATAAAC
TGTTTGCTTGATGCATGTATTTTCTTCCAGCTCTGTTCCGCACGTAAGCATCCTGCTTCTG
CCAGATCAACTCTGTCTGTGAGCAATAGTTGAACTTTATGTACATAGAGAAATAGATA
ATACAATATTACATTACAGCCTGTATTCAATTTGTTCTCTAGAAGTTTTGTGAGAAATTTGAC
TTGTTGACATAAATTTGTAATGCATATATACAATTTGAAGCACTCCTTTTCTTCAGTTCCTC
AGCTCCTCTCATTTTCAAGCAATATCCATTTTCAAGGTGCAGAACAAAGGAGTGAAAGAAAATA
TAAGAAGAAAAAATCCCCTACATTTTATTGGCACAGAAAAGTATTAGGTGTTTTTCTTAGT
GGAATATTAGAAATGATCATATTCATTATGAAAGGTCAAGCAAAGACAGCAGAATACCAATC
ACTTCATCATTTAGGAAGTATGGGAACTAAGTTAAGGAAGTCCAGAAAGAAGCCAAGATATA
TCCTTATTTTCATTTCCAAACAACACTATGATAAATGTGAAGAAGATTCTGTTTTTTTGTG
ACCTATAATAATTATACAACTTCATGCAATGTACTTGTCTAAGCAAATTAAAGCAAATAT
TTATTTAACATTGTTACTGAGGATGTCAACATATAACAATAAAATATAAATCACCCA

FIGURE 150

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68871

><subunit 1 of 1, 423 aa, 1 stop

><MW: 47696, pI: 8.96, NX(S/T): 3

MMYRPDVVRARKRVCWEPWVIGLVIFISLIVLAVCIGLTVHYVRYNQKKTYNYSTLSFTTD
KLYAEFGREASNNFTEMSQRLESMVKNAFYKSPLREEFVKSQVIKFSQQKHGVLAHMLLICR
FHSTEDPETVDKIVQLVLHEKLQDAVGPPKVDPHSVKIKKINKTETDSYLNHCCGTRRSKTL
GQSLRIVGGTEVEEGEWPWQASLQWDGSHRCGATLINATWLVSAAHCFTTYKNPARWTASFG
VTIKPSKMKRGLRRIIVHEKYKHPSHDYDISLAELSSVPYTNVHRVCLPDASYEFQPGDV
MFVTGFGALKNDGYSQNHRLRQAQVTLIDATTCNEPQAYNDAITPRMLCAGSLEGKTDACQGD
SGGPLVSSDARDIWIYLAGIVSWGDECAKPNKPGVYTRVTALRDWITSKTGI

Transmembrane domain:

amino acids 21-40 (type II)

FIGURE 151

GTCGAAGGTTATAAAAGCTTCCAGCCAAACGGCATTGAAGTTGAAGATACAACCTGACAGCA
CAGCCTGAGATCTTGGGGATCCCTCAGCCTAACACCCACAGACGTCAGCTGGTGGATTCCCG
CTGCATCAAGGCCTACCCACTGTCTCCATGCTGGGCTCTCCCTGCCTTCTGTGGCTCCTGGC
CGTGACCTTCTTGGTTCCCAGAGCTCAGCCCTTGGCCCCCTCAAGACTTTGAAGAAGAGGAGG
CAGATGAGACTGAGACGGCGTGGCCGCCTTTGCCGGCTGTCCCCTGCGACTACGACCACTGC
CGACACCTGCAGGTGCCCTGCAAGGAGCTACAGAGGGTCGGGCCGGCGGCCTGCCTGTGCCC
AGGACTCTCCAGCCCCGCCAGCCGCCGACCCGCCGCGCATGGGAGAAGTGCGCATTGCGG
CCGAAGAGGGCCGCGCAGTGGTCCACTGGTGTGCCCCCTTCTCCCCGGTCTCTCACTACTGG
CTGCTGCTTTGGGACGGCAGCGAGGCTGCGCAGAAGGGGCCCCCGCTGAACGCTACGGTCCG
CAGAGCCGAAGTGAAGGGGCTGAAGCCAGGGGGCATTATGTCGTTTGCGTAGTGGCCGCTA
ACGAGGCCGGGGCAAGCCGCGTGCCCCAGGCTGGAGGAGAGGGCCTCGAGGGGGCCGACATC
CCTGCCTTCGGGCCTTGCAAGCCGCTTGCGGTGCCGCCAACCCCCGCACTCTGGTCCACGC
GGCCGTCGGGGTGGGCACGGCCCTGGCCCTGCTAAGCTGTGCCGCCCTGGTGTGGCACTTCT
GCCTGCGCGATCGCTGGGGCTGCCCCGCGCCGAGCCGCCGCCGAGCCGCAGGGGGCGCTCTTGA
AAGGGGCCTGGGGGCATCTCGGGCACAGACAGCCCCACCTGGGGCGCTCAGCCTGGCCCCCG
GGAAAGAGGAAAACCCGCTGCCTCCAGGGAGGGCTGGACGGCGAGCTGGGAGCCAGCCCCAG
GCTCCAGGGCCACGGCGGAGTCATGGTTCTCAGGACTGAGCGCTTGTTTAGGTCCGGTACTT
GGCGCTTTGTTTCCTGGCTGAGGTCTGGGAAGGAATAGAAAGGGGCCCCCAATTTTTTTTTTA
AGCGGCCAGATAATAAATAATGTAACCTTTGCGGTTAAAAAAAAAAAAAAAAAAAA

FIGURE 152

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68874

><subunit 1 of 1, 238 aa, 1 stop

><MW: 25262, pI: 6.44, NX(S/T): 1

MLGSPCLLWLLAVTFLVPRAQPLAPQDFEEEEADETETAWPPLPAVPCDYDHCRLQVPCKE
LQRVGPAACLCPLGLSSPAQPPDPPEMGEVRIAAEEGRAVVHWCAPFSPVLHYWLLLWDGSEA
AQKGPPLNATVRRRAELKGLKPGGIYVVCVVAANEAGASRVPPQAGGEGLEGADIPAFGPCSRL
AVPPNPRTLVAHAVGVGTALALLSCAALVWHFCLRDWRWGCPRRRAARAAGAL

Important features of the protein:

Signal peptide:

amino acids 1-20

Transmembrane domain:

amino acids 194-220

N-glycosylation site.

amino acids 132-135

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FIGURE 153

AGAGAAAGAAGCGTCTCCAGCTGAAGCCAATGCAGCCCTCCGGCTCTCCGCGAAGAAGTTCC
CTGCCCCGATGAGCCCCGCGTGCGTCCCCGACTATCCCCAGGCGGGCGTGGGGCACC GGG
CCCAGCGCCGACGATCGCTGCCGTTTTGCCCTTGGGAGTAGGATGTGGTGAAAGGATGGGGC
TTCTCCCTTACGGGGCTCACAATGGCCAGAGAAGATTCCGTGAAGTGTCTGCGCTGCCTGCT
CTACGCCCTCAATCTGCTCTTTTGGTTAATGTCCATCAGTGTGTTGGCAGTTTCTGCTTGGA
TGAGGGACTACCTAAATAATGTTCTCACTTTAACTGCAGAAACGAGGGTAGAGGAAGCAGTC
ATTTTGACTTACTTTCTGTGGTTTCATCCGGTCATGATTGCTGTTTGCTGTTTCTTATCAT
TGTGGGGATGTTAGGATATTGTGGAACGGTGAAAAGAAATCTGTTGCTTCTTGCATGGTACT
TTGGAAGTTTGCTTGTCATTTTCTGTGTAGAACTGGCTTGTGGCGTTTGGACATATGAACAG
GAACTTATGGTTCCAGTACAATGGTCAGATATGGTCACTTTGAAAGCCAGGATGACAAATTA
TGGATTACCTAGATATCGGTGGCTTACTCATGCTTGGAAATTTTTTTTCAGAGAGAGTTTAAGT
GCTGTGGAGTAGTATATTTCACTGACTGGTTGGAAATGACAGAGATGGACTGGCCCCCAGAT
TCCTGCTGTGTTAGAGAATTCCCAGGATGTTCCAAACAGGCCCACCAGGAAGATCTCAGTGA
CCTTTATCAAGAGGGTTGTGGGAAGAAAATGTATTCCTTTTTGAGAGGAACCAACAACCTGC
AGGTGCTGAGGTTTCTGGGAATCTCCATTGGGGTGACACAAATCCTGGCCATGA[†]TCTCACC
ATTACTCTGCTCTGGGCTCTGTATTATGATAGAAGGGAGCCTGGGACAGACCAAAATGATGTC
CTTGAAGAATGACAACTCTCAGCACCTGTCTGTCCTCAGTAGAACTGTTGAAACCAAGCC
TGTCAAGAATCTTTGAACACACATCCATGGCAAACAGCTTTAATACACACTTTGAGATGGAG
GAGTTATTAAAAAGAAATGTCACAGAAGAAAACCACAAACTTGTTTTATTGGACTTGTGAATT
TTTGAGTACATACTATGTGTTTTCAGAAATATGTAGAAATAAAAATGTTGCCATAAAATAACA
CCTAAGCATATACTATTCTATGCTTTAAAATGAGGATGGAAAAGTTTCATGTCTAAGTCAC
CACCTGGACAATAATTGATGCCCTTAAAATGCTGAAGACAGATGTCATACCCACTGTGTAGC
CTGTGTATGACTTTTACTGAACACAGTTATGTTTTGAGGCAGCATGGTTTGATTAGCATTTC
CGCATCCATGCAAACGAGTCACATATGGTGGGACTGGAGCCATAGTAAAGGTTGATTTACTT
CTACCAACTAGTATATAAAGTACTAATTAATGCTAACATAGGAAGTTAGAAAATACTAATA
ACTTTTATTACTCAGCGATCTATTCTTCTGATGCTAAATAAATTATATATCAGAAAACCTTC
AATATTGGTGACTACCTAAATGTGATTTTTGCTGGTTACTAAAATATTCTTACCACTTAAAA
GAGCAAGCTAACACATTGTCTTAAGCTGATCAGGGATTTTTTGTATATAAGTCTGTGTTAAA
TCTGTATAATTCAGTCGATTTTCACTTCTGATAATGTTAAGAATAACCATTATGAAAAGGAAA
ATTTGTCCTGTATAGCATCATTATTTTTAGCCTTTCCTGTTAATAAAGCTTTACTATTCTGT
CCTGGGCTTATATTACACATATAACTGTTATTTAAATACTTAACCACTAATTTTGAAAATTA
CCAGTGTGATACATAGGAATCATTATTCAGAATGTAGTCTGGTCTTTAGGAAGTATTAATAA
GAAAATTTGCACATAACTTAGTTGATTCAGAAAGGACTTGTATGCTGTTTTTCTCCCAAATG
AAGACTCTTTTTTGACACTAAACACTTTTTTAAAAGCTTATCTTTGCCTTCTCCAAACAAGAA
GCAATAGTCTCCAAGTCAATATAAATTCTACAGAAAATAGTGTCTTTTTTCTCCAGAAAAAT
GCTTGTGAGAATCATTAAAACATGTGACAATTTAGAGATTCTTTGTTTTATTTCACTGATTA
ATATACTGTGGCAAATTACACAGATTATTAAATTTTTTTTACAAGAGTATAGTATATTTATTT
GAAATGGGAAAAGTGCATTTTACTGTATTTTGTGTATTTTGTATTATTTCTCAGAATATGGAA
AGAAAATTAAAATGTGTCAATAAATATTTTCTAGAGAGTAA

FIGURE 154

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68880

><subunit 1 of 1, 305 aa, 1 stop

><MW: 35383, pI: 5.99, NX(S/T): 0

MAREDSVKCLRCLLYALNLLFWLMSISVLAVSAWMRDYLNNVLTTLTAETRVEEAVILTYFPV
VHPVMIAVCCFLIIVGMLGYCGTVKRNLLLLAWYFGSLLVIFCVELACGVWTYEQELMVPVQ
WSDMVTLKARMTNYGLPRYRWLTHAWNFFQREFKCCGVVYFTDWLEMTMDWPPDSCCVREF
PGCSKQAHQEDLSDLYQEGCGKKMYSFLRGTKQLQVLRFLGISIGVTQILAMILTITLLWAL
YYDRREPGTDQMMSLKNDNSQHLSCPSVELLKPSLSRIFEHTSMANSFNTHFEMEEL

Signal peptide:

amino acids 1-33

Transmembrane domains:

amino acids 12-35, 57-86, 94-114, 226-248

FIGURE 155

GAGAGAGGCAGCAGCTTGCTCAGCGGACAAGGATGCTGGGCGTGAGGGACCAAGGCCTGCCC
TGCACTCGGGCCTCCTCCAGCCAGTGCTGACCAGGGACTTCTGACCTGCTGGCCAGCCAGGA
CCTGTGTGGGGAGGCCCTCCTGCTGCCTTGGGGTGACAATCTCAGCTCCAGGCTACAGGGAG
ACCGGGAGGATCACAGAGCCAGCATGTTACAGGATCCTGACAGTGATCAACCTCTGAACAGC
CTCGATGTCAAACCCCTGCGCAAACCCCGTATCCCCATGGAGACCTTCAGAAAGGTGGGGAT
CCCCATCATCATAGCACTACTGAGCCTGGCGAGTATCATCATTGTGGTTGTCTCATCAAGG
TGATTCTGGATAAATACTACTTCCCTCTGCGGGCAGCCTCTCCACTTCATCCCAGGAAGCAG
CTGTGTGACGGAGAGCTGGACTGTCCCTTGGGGGAGGACGAGGAGCACTGTGTCAAGAGCTT
CCCCGAAGGGCCTGCAGTGGCAGTCCGCCTCTCCAAGGACCGATCCACACTGCAGGTGCTGG
ACTCGGCCACAGGGAACTGGTTCTCTGCCTGTTTTGACAACCTTCACAGAAGCTCTCGCTGAG
ACAGCCTGTAGGCAGATGGGCTACAGCAGAGCTGTGGAGATTGGCCCAGACCAGGATCTGGA
TGTTGTTGAAATCACAGAAAACAGCCAGGAGCTTCGCATGCGGAACTCAAGTGGGCCCTGTC
TCTCAGGCTCCCTGGTCTCCCTGCACTGTCTTGCTGTGGGAAGAGCCTGAAGACCCCCCGT
GTGGTGGGTGGGGAGGAGGCCTCTGTGGATTCTTGGCCTTGGCAGGTCAGCATCCAGTACGA
CAAACAGCACGTCTGTGGAGGGAGCATCCTGGACCCCCACTGGGTCTCACGGCAGCCCACT
GCTTCAGGAAACATAACCGATGTGTTCAACTGGAAGGTGCGGGCAGGCTCAGACAAACTGGGC
AGCTTCCCATCCCTGGCTGTGGCCAAGATCATCATCATTGAATTCAACCCCATGTACCCCAA
AGACAATGACATCGCCCTCATGAAGCTGCAGTTCCCACTCACTTTCTCAGGCACAGTCAGGC
CCATCTGTCTGCCCTTCTTTGATGAGGAGCTCACTCCAGCCACCCCACTCTGGATCATTGGA
TGGGGCTTTACGAAGCAGAATGGAGGGGAAGATGTCTGACATACTGCTGCAGGCGTCAGTCCA
GGTCATTGACAGCACACGGTGCAATGCAGACGATGCGTACCAGGGGGAAGTCACCGAGAAGA
TGATGTGTGCAGGCATCCCGGAAGGGGGTGTGGACACCTGCCAGGGTGACAGTGGTGGGCCC
CTGATGTACCAATCTGACCAGTGGCATGTGGTGGGCATCGTTAGCTGGGGCTATGGCTGCGG
GGGCCCCGAGCACCCCAAGGAGTATACACCAAGGTCTCAGCCTATCTCAACTGGATCTACAATG
TCTGGAAGGCTGAGCTGTAATGCTGCTGCCCCCTTTGCAGTGCTGGGAGCCGCTTCCTTCCTG
CCCTGCCCACCTGGGGATCCCCCAAAGTCAGACACAGAGCAAGAGTCCCCTTGGGTACACCC
CTCTGCCCACAGCCTCAGCATTTCTTGGAGCAGCAAAGGGCCTCAATTCCTGTAAGAGACCC
TCGCAGCCCAGAGGCGCCCAGAGGAAGTCAGCAGCCCTAGCTCGGCCACACTTGGTGCTCCC
AGCATCCCAGGGAGAGACACAGCCCACTGAACAAGGTCTCAGGGGTATTGCTAAGCCAAGAA
GGAACCTTTCCCACACTACTGAATGGAAGCAGGCTGTCTTGTAAGGCCAGATCACTGTGGG
CTGGAGAGGAGAAGGAAAGGGTCTGCGCCAGCCCTGTCCGTCTTCACCCATCCCCAAGCCTA
CTAGAGCAAGAAACAGTTGTAATATAAAATGCACTGCCCTACTGTTGGTATGACTACCGTT
ACCTACTGTTGTCAATTGTTATTACAGCTATGGCCACTATTATTAAAGAGCTGTGTAACATCT
CTGGCAAAAAAAAAAAAA

FIGURE 156

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68885

><subunit 1 of 1, 432 aa, 1 stop

><MW: 47644, pI: 5.18, NX(S/T): 2

MLQDPDSDQPLNSLDVKPLRKPRIPMETFRKVGIPIIIIALLSLASIIIVVVLIKVILDKYYF
LCGQPLHFIPRKQLCDGELDCPLGEDEEHCVKSFPEGPAVAVRLSKDRSTLQVLDSATGNWF
SACFDNFTEALAEACRQMGYSRAVEIGPDQDLVDVEITENSQELMRNSSGPCLSGSLVSL
HCLACGKSLKTPRVVGEEASVDSWPWQVSIQYDKQHVCSSILDPHWLTAAHCFRKHTDV
FNWKVRAGSDKLGSFPSLAVAKIIIIIEFNPMYPKDNDIALMKLQFPLTFSGTVRPICLPFFD
EELTPATPLWIIIGWGFTKQNGGKMSDILLQASVQVIDSTRCNADDAYQGEVTEKMMCAGIPE
GGVDTCQGDSGGPLMYQSDQWHVVGIVSWGYGCGGPSTPGVYTKVSAYLNWIYNVWKAEL

Transmembrane domain:

amino acids 32-53 (typeII)

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FIGURE 157

GGGCTGAGGCACTGAGAGACCGGAAAGCCTGGCATTCCAGAGGGAGGGAAACGCAGCGGCATCCCCAGGCTCCAG
AGCTCCCTGGTGACAGTCTGTGGCTGAGCATGGCCCTCCCAGCCCTGGGCCCTGGACCCCTGGAGCCTCCTGGGCC
TTTTCTCTTCCAAGTCTTCAGCTGCTGCTGCCGACGACGACCGCGGGGGAGGCGGGCAGGGGCCCATGCCCA
GGGTGAGATACTATGCAGGGGATGAACGTAGGGCACTTAGCTTCTTCCACCAGAAGGGCCTCCAGGATTTTGACA
CTCTGCTCCTGAGTGGTGATGGAATACTCTCTACGTGGGGGCTCGAGAAGCCATTCTGGCCTTGATATCCAGG
ATCCAGGGGTCCCCAGGCTAAAGAACATGATACCGTGGCCAGCCAGTGACAGAAAAAGAGTGAATGTGCCTTTA
AGAAGAAGAGCAATGAGACACAGTGTTCACCTTCATCCGTGTCTGGTTTCTTACAATGTACCCATCTCTACA
CCTGCGGCACCTTCGCCTTCAGCCCTGCTTGTACCTTCATTGAACCTCAAGATTCTACCTGTTGCCCATCTCGG
AGGACAAGGTCATGGAGGGGAAAAAGGCCAAAGCCCCCTTGACCCCGCTCACAAGCATACGGCTGTCTTGGTGGATG
GGATGCTCTATTCTGGTACTATGAACAACCTTCCTGGGCAGTGAGCCCATCTGTATGCGCACACTGGGATCCCAGC
CTGTCTCAAGACCGACAACCTTCCTCCGCTGGCTGCATCATGACGCCCTCCTTTGTGGCAGCCATCCCTTCGACCC
AGGTCGTCTACTTCTTCTTCGAGGAGACAGCCAGCGAGTTTGACTTCTTTGAGAGGCTCCACACATCGCGGTGG
CTAGAGTCTGCAAGAATGACGTGGGCGGCGAAAAAGCTGCTGCAGAAGAAGTGGACCACCTTCCTGAAGGCCAGC
TGCTCTGCACCCAGCCGGGGCAGCTGCCCTTCAACGTCTATCCGCCACGCGGTCTGTCTCCCGCCGATTCCTCCA
CAGCTCCCCACATCTACGCAGTCTTCACCTCCCACTGGCAGGTTGGCGGGACCAAGGAGCTCTGCGGTTTGTGCCT
TCTCTCTCTTGACATTGAACGTGTCTTTAAGGGGAAATACAAAGAGTTGAACAAAGAACTTCACGCTGGACTA
CTTATAGGGGCCCTGAGACCAACCCCCGGCCAGGCAGTTGCTCAGTGGGCCCCCTCCTCTGATAAGGCCCTGACCT
TCATGAAGGACCATTTCCTGATGGATGAGCAAGTGGTGGGGACGCCCTGCTGGTGAAATCTGGCGTGGAGTATA
CACGGCTTGCAAGTGGAGACAGCCAGGGCCTTGATGGGCACAGCCATCTTGTATGTACCTGGGAACCACCACAG
GGTCGCTCCACAAGGCTGTGGTAAGTGGGGACAGCAGTGTCTCATCTGGTGGAAGAGATTGAGCTGTTCCCTGACC
CTGAACCTGTTTCGCAACCTGCAGCTGGCCCCCACCCAGGGTGCAGTGTCTGTAGGCTTCTCAGGAGGTGTCTGGA
GGGTGCCCCGAGCCAACTGTAGTGTCTATGAGAGCTGTGTGGACTGTGTCTTGGCCGGGACCCCCACTGTGCCT
GGGACCCTGAGTCCCGAACCTGTTGCCTCCTGTCTGCCCCAACCTGAACCTCTGGAAGCAGGACATGGAGCGGG
GGAACCCAGAGTGGGCATGTGCCAGTGGCCCCATGAGCAGGAGCCTTCGGCCTCAGAGCCGCCCCGAAATCATTA
AAGAAGTCTGGCTGTCCCCAACTCCATCCTGGAGCTCCCCTGCCCCACCTGTGAGCCTTGGCCTCTTATTATT
GGAGTCATGGCCAGCAGCAGTCCAGAAGCCTCTTCACTGTCTACAATGGCTCCCTCTTGTGATAGTGCAGG
ATGGAGTTGGGGGTCTCTACCAAGTGTGGGCAACTGAGAATGGCTTTTCATACCCTGTGATCTCCTACTGGGTGG
ACAGCCAGGACCAGACCCTGGCCCTGGATCCTGAACCTGGCAGGCATCCCCCGGGAGCATGTGAAGGTCCCGTTGA
CCAGGGTCAGTGGTGGGGCCGCCCTGGCTGCCAGCAGTCTTACTGGCCCCACTTTGTCACTGTCACTGTCTCTCT
TTGCCTTAGTGCTTTCAGGAGCCCTCATCATCTCTGCTGGCCTCCCCATTGAGAGCACTCCGGGCTCGGGGCAAGG
TTCAGGGCTGTGAGACCCCTGCGCCCTGGGGAGAAGGCCCGTTAAGCAGAGAGCAACACCTCCAGTCTCCCAAGG
AATGCAGGACCTCTGCCAGTGTGTGGACGCTGACAACAACCTGCCTAGGCAGTGGGTAGCTTAAACTCTAGGCA
CAGGCCGGGGCTGCGGTGCAGGCACCTGGCCATGTCTGGCTGGGCGGCCCAAGCACAGCCCTGACTAGGATGACAG
CAGCACAAAAGACCACCTTTCTCCCCTGAGAGGAGCTTCTGCTACTCTGCATCACTGATGACACTCAGCAGGGTG
ATGCACAGCAGTCTGCCTCCCCTATGGGACTCCCTTCTACCAAGCACATGAGCTCTCTAACAGGGTGGGGGCTAC
CCCCAGACCTGCTCCTACACTGATATTGAAGAACCTGGAGAGGATCCTTCAGTTCTGGCCATTCCAGGGACCCCTC
CAGAAACACAGTGTTCAGAGACCCCTAAAAAACCTGCCTGTCCAGGACCCCTATGGTAATGAACACCAACATC
TAAACAATCATATGCTAACATGCCACTCCTGGAAACTCCACTCTGAAGCTGCCGCTTTGGACACCAACACTCCCT
TCTCCCAGGGTCATGCAGGGATCTGCTCCCTCCTGCTTCCCTTACCAGTCGTGCACCGCTGACTCCCAGGAAGTC
TTTCTGAAGTCTGACCACCTTTCTTCTTCTGCTTTCAGTTGGGGCAGACTCTGATCCCTTCTGCCCTGGCAGAATGG
CAGGGGTAATCTGAGCCTTCTTCACTCCTTTACCCTAGCTGACCCCTTCACCTCTCCCCCTCCCTTTTCTTTGT
TTTGGGATTCAGAAAACCTGCTTGTGAGAGACTGTTTATTTTTTTATTAATAAGGCTTAAAAAA

FIGURE 158

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71166
><subunit 1 of 1, 761 aa, 1 stop
><MW: 83574, pI: 6.78, NX(S/T): 4
MALPALGLDPWSSLGLFLFQLQLLLPTTTAGGGGQGMPRVRYAGDERRALSFFHQKGLQ
DFDTLLLSGDGNTLYVGAREAILALDIQDPGVPRLNMIWPASDRKKSECAFKKKSNETQC
FNFIRVLVSYNVTHLYTCGTFAFSPACTFIELQDSYLLPISEDKVMEGKGQSPFDPAHKHTA
VLVDGMLYSGTMNNFLGSEPILMRTLGSQPVLKTDNFLRWLHHDASFVAAIPSTQVVYFFFE
ETASEFDDFERLHTSRVARVCKNDVGGEKLLQKKWTTFLKAQLLCTQPGQLPFNVIRHAVLL
PADSPTAPHIYAVFTSQWQVGGTRSSAVCAFSLLDIERVFKGKYKELNKETSRWTTYRGPET
NPRPGSCSVGPSSDKALTFMKDHFLMDEQVVGTPLLVKSGVEYTRLAVETAQGLDGHSHLVM
YLGTTTGS LHKAVVSGDSSAHLVEEIQLFDPPEPVRNLQLAPTQGAVFVGFSGGVWRVP
RANCSVYESCVDCVLARDPHCAWDPESTRCCLLSAPNLNSWKQDMERGNPEWACASGPM
SRSLRPQSRPQIIKEVLAVPNSILELPCPHLSALASYWSHGPAAVPEASSTVYNGSLLL
IVQDGVGGLYQCWATENGFSYPVISYWVDSQDQTLALDPELAGIPREHVKVPLTRVSGGA
ALAAQQSYWPHFVTVTVLFAVLVSGALIILVASPLRALRARGKVQGCETLRPGEKAPLSRE
QHLQSPKECRTSASDVDADNNCLGTEVA

Signal peptide:

amino acids 1-30

Transmembrane domains:

amino acids 136-156, 222-247, 474-490, 685-704

FIGURE 159

AGGGTCCCTTAGCCGGGCGCAGGGCGCGCAGCCCAGGCTGAGATCCGCGGCTTCCGTAGAAG
TGAGCATGGCTGGGCAGCGAGTGCTTCTTCTAGTGGGCTTCCTTCTCCCTGGGGTCCTGCTC
TCAGAGGCTGCCAAAATCCTGACAATATCTACAGTAGGTGGAAGCCATTATCTACTGATGGA
CCGGGTTTCTCAGATTCTTCAAGATCACGGTCATAATGTCAACCATGCTTAACCACAAAAGAG
GTCCTTTTATGCCAGATTTTAAAAAGGAAGAAAAATCATATCAAGTTATCAGTTGGCTTGCA
CCTGAAGATCATCAAAGAGAATTTAAAAAGAGTTTTGATTTCTTTCTGGAAGAACTTTAGG
TGGCAGAGGAAAATTTGAAAACCTATTAAATGTTCTAGAATACTTGGCGTTGCAGTGCAGTC
ATTTTTTAAATAGAAAGGATATCATGGATTCTTAAAGAATGAGAAGCTTCGACATGGTGATA
GTTGAAACTTTTGACTACTGTCTTTCTTGATTGCTGAGAAGCTTGGGAAGCCATTTGTGGC
CATTCTTTCCACTTCATTGGGCTCTTTGGAATTTGGGCTACCAATCCCCTTGTCTTATGTTT
CAGTATTCCGTTCCCTTGCTGACTGATCACATGGACTTCTGGGGCCGAGTGAAGAATTTTCTG
ATGTTCTTTAGTTTCTGCAGGAGGCAACAGCACATGCAGTCTACATTTGACAACACCATCAA
GGAACATTTACAGAAGGCTCTAGGCCAGTTTTGTCTCATCTTCTACTGAAAGCAGAGTTGT
GGTTCATTAACCTGACTTTGCCTTTGATTTTGCTCGACCTCTGCTTCCCAACACTGTTTAT
GTTGGAGGCTTGATGGAAAACCTATTAAACCAGTACCACAAGACTTGGAGAAGCTTCATTGC
CAAGTTTGGGGACTCTGGTTTTGTCTTGACCTTGGGCTCCATGGTGAACACCTGTGAGA
ATCCGGAATCTTCAAGGAGATGAACAATGCCTTTGCTCACCTACCCCAAGGGGTGATATGG
AAGTGTGAGTGTCTCATTGGCCCAAAGATGTCCACCTGGCTGCAAATGTGAAAATTTGTGGA
CTGGCTTCCTCAGAGTGACCTCCTGGCTCACCCAAGCATCCGTCTGTTTTGTACCCACGGCG
GGCAGAATAGCATAATGGAGGCCATCCAGCATGGTGTGCCCATGGTGGGGATCCCTCTCTTT
GGAGACCAGCCTGAAAACATGGTCCGAGTAGAAGCCAAAAAGTTTGGTGTCTTCTATTCAGTT
AAAGAAGCTCAAGGCAGAGACATTGGCTCTTAAGATGAAACAAATCATGGAAGACAAGAGAT
ACAAGTCCGCGGCAGTGGCTGCCAGTGTATCCTGCGCTCCCACCCGCTCAGCCCCACACAG
CGGCTGGTGGGCTGGATTGACCACGTCTCCAGACAGGGGGCGCGACGCACCTCAAGCCCTA
TGTCTTTCAGCAGCCCTGGCATGAGCAGTACCTGTTGACGTTTTTGTGTTTTCTGCTGGGGC
TCACTCTGGGGACTCTATGGCTTTGTGGGAAGCTGCTGGGCATGGCTGTCTGGTGGCTGCGT
GGGGCCAGAAAGGTGAAGGAGACATTAAGGCCAGGTGCAGCCTTGGCGGGGTCTGTTTGGTGG
GCGATGTCAACATTTCTAGGGAGCTTCCCACTAGTTCTGGCAGCCCCATTCTCTAGTCCTTC
TAGTTATCTCCTGTTTTCTTGAAGAACAGGAAAAATGGCCAAAAATCATCCTTTCCACTTGC
TAATTTTGCTACAAATTCATCCTTACTAGCTCCTGCCTGCTAGCAGAAATCTTTCCAGTCCT
CTTGTCTCCTTTGTTTGCCATCAGCAAGGGCTATGCTGTGATTCTGTCTCTGAGTGAAGT
GACCACTGACCCTCAGATTTCCAGCCTTAAAATCCACCTTCCTTCTCATGCGCTCTCCGAA
TCACACCTGACTCTTCCAGCCTCCATGTCCAGACCTAGTCAGCCTCTCTCACTCCTGCCCC
TACTATCTATCATGGAATAACATCCAAGAAAGACACCTTGCAATTTCTTTCAGTTTCTGTTT
TGTTCTCCACATATTCTCTTCAATGCTCAGGAAGCCTGCCCTGTGCTTGAGAGTTTCAAGGC
CGGACACAGGCTCACAGGTCTCCACATTGGGTCCCTGTCTCTGGTGCCACAGTGAGCTCCT
TCTTGGCTGAGCAGGCATGGAGACTGTAGGTTTCCAGATTTCTTGAAAAATAAAAGTTTACA
GCGTTATCTCTCCCAACCTCACTAA

FIGURE 160

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71169

><subunit 1 of 1, 523 aa, 1 stop

><MW: 59581, pI: 8.68, NX(S/T): 1

MAGQRVLLLVGFLLPGVLLSEAAKILTISTVGGSHYLLMDRVSQILQDHGHNVTMLNHKRG
FMPDFKKEEKSYQVISWLAPEDHQREFKKSFDFFLEETLGGRGKFENLLNVLEYLALQCSHF
LNRKDIMDSLKNENFDMVIVETFDYCPFLIAEKLKPKFVAILSTSFGSLEFGLPIPLSYVPV
FRSLTLDHMDFWGRVKNFLMFFSFCRRQQHMQSTFDNTIKEHFTEGSRPVLSHLLLKAELWF
INSDFAFDFAARPLLNTVYVGGLMEKPIKPVPQDLENFIAKFGDSGFVLVTLGSMVNTCQNP
EIFKEMNNAFAHLPQGVWKCQCSHWPKDVHLAANVKIVDWLPQSDLLAHPSIRLFVTHGGQ
NSIMEAIIQHGVPVMVGIPFLFGDQPENMVRVEAKKFGVSIQLKKLKAETLALKMKQIMEDKRYK
SAAVAASVILRSHPLSPTQRLVGWIDHVLQTTGATHLKPYVFQQPWHEQYLFDFVVFLLGLT
LGTLLWLCGKLLGMAVWWLRGARKVKET

Signal peptide:

amino acids 1-19

Transmembrane domain:

amino acids 483-504

162/270

FIGURE 161

GGGCTGTTGATTTGTGGGGGATTTTGAAGAGAGGAGGAATAGGAGGAAGGGGTTGAGGGGCT
GCCTCTGGCATATGCACACACTCACACATTCTGTACACCCGTCACACACACATACCATGTT
CTCCATCCCCCAGGTCCAGCCCTCAGTGCTGTCCCATCCAGCAGGGCTACCCTGAAGCTCT
GGCTGCAGCCCTCCCGTCCAGTGGGCAGGCGGCTTCATCCCTCCTTTCTCTCCCAAAGCCCA
ACTGCTGTCACTGCATGCTCTGCCAAGGAGGAGGGAAGTGCAGTGACAGCAGGAGTAAGAGT
GGGAGGCAGGACAGAGCTGGGACACAGGTATGGAGAGGGGGTTTCAGCGAGCCTAGAGAGGGC
AGACTATCAGGGTGCCGGCGGTGAGAATCCAGGGAGAGGAGCGGAAACAGAAGAGGGGCAGA
AGACCGGGGCACTTGTGGGTTGCAGAGCCCTCAGCCATGTTGGGAGCCAAGCCACACTGGC
TACCAGGTCCCCTACACAGTCCCGGGCTGCCCTTGGTTCTGGTGCTTCTGGCCCTGGGGGCC
GGGTGGGCCCAGGAGGGGTTCAGAGCCCGTCTGCTGGAGGGGGAGTGCCTGGTGGTCTGTGA
GCCTGGCCGAGCTGCTGCAGGGGGGCCCCGGGGGAGCAGCCCTGGGAGAGGCACCCCTGGGC
GAGTGGCATTTGCTGCGGTCCGAAGCCACCACCATGAGCCAGCAGGGGAAACCGGCAATGGC
ACCAGTGGGGCCATCTACTTCGACCAGGTCTGGTGAACGAGGGCGGTGGCTTTGACCGGGC
CTCTGGCTCCTTCGTAGCCCCCTGTCCGGGGTGTCTACAGCTTCCGGTTCCATGTGGTGAAGG
TGTACAACCGCCAACTGTCCAGGTGAGCCTGATGCTGAACACGTGGCCTGTCTCTCAGCC
TTTGCCAATGATCCTGACGTGACCCGGGAGGCAGCCACCAGCTCTGTGCTACTGCCCTTGA
CCCTGGGGACCGAGTGTCTCTGCGCCTGCGTCGGGGGAATCTACTGGGTGGTTGGAAATACT
CAAGTTTCTCTGGCTTCCTCATCTTCCCTCTCTGAGGACCCCAAGTCTTTCAAGCACAAGAAT
CCAGCCCCTGACAACTTTCTTCTGCCCTCTCTTGCCCCAGAAACAGCAGAGGCAGGAGAGAG
ACTCCCTCTGGCTCCTATCCACCTCTTTGCATGGGACCCTGTGCCAAACACCCCAAGTTTAA
GAGAAGAGTAGAGCTGTGGCATCTCCAGACCAGGCCTTTCCACCCACCCACCCCCAGTTACC
CTCCCAGCCACCTGCTGCATCTGTTCTGCTGCAGCCCTAGGATCAGGGCAAGGTTTGGCA
AGAAGGAAGATCTGCACTACTTTGCGGCCTCTGCTCCTCCGGTTCCCCCACCCAGCTTCCT
GCTCAATGCTGATCAGGGACAGGTGGCGCAGGTGAGCCTGACAGGCCCCCACAGGAGCCAG
ATGGACAAGCCTCAGCGTACCCTGCAGGCTTCTTCTGTGAGGAAAGCCAGCATCACGGATC
TCAGCCAGCACCGTCAGAAGCTGAGCCAGCACCGTATGGGCTAGGGTGGGAGGCTCAGCCAC
AGGCAGAAGGGTGGGAAGGGCCTGGAGTCTGTGGCTGGTGAGGAAGGAAGGAGGGTGTATTG
TCTAGACTGAACATGGTACACATTCTGCATGTATAGCAGAGCAGCCAGCAGGTAGCAATCCT
GGCTGTCCTTCTATGCTGGATCCCAGATGGACTCTGGCCCTTACCTCCCCACCTGAGATTAG
GGTGAGTGTGTTTGCTCTGGCTGAGAGCAGAGCTGAGAGCAGGTATACAGAGCTGGAAGTGG
ACCATGGAAAACATCGATAACCATGCATCCTCTTGCTTGGCCACCTCCTGAAACTGCTCCAC
CTTTGAAGTTTGAACTTTAGTCCCTCCACACTCTGACTGCTGCCTCCTTCTCTCCAGCTCTC
TCACTGAGTTATCTTCACTGTACCTGTTCCAGCATATCCCCACTATCTCTCTTTCTCTGAT
CTGTGCTGTCTTATTCTCCTCCTTAGGCTTCTATTACCTGGGATTCCATGATTCAATCCTT
CAGACCTCTCCTGCCAGTATGCTAAACCTCCCTCTCTCTTTCTTATCCCGCTGTCCATT
GGCCCAGCCTGGATGAATCTATCAATAAAACAAGTAGAGAATGGTGGTCAGTGAGACACTAT
AGAATTACTAAGGAGAAGATGCCTCTGGAGTTTGGATCGGGTGTTACAGGTACAAGTAGGTA
TGTTGCAGAGGAAAATAAATATCAAACCTGTATACTAAAATTAAAAA

FIGURE 162

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71180

><subunit 1 of 1, 205 aa, 1 stop

><MW: 21521, pI: 7.07, NX(S/T): 1

MLGAKPHWLPGPLHSPGLPLVLVLLALGAGWAQEGSEPVLLLEGECLVVCEPGRAAAGGPGGA
ALGEAPPGRVAFAAVRSHHHEPAGETGNGTSGAIYFDQVLVNEGGGFDRASGSFVAPVRGVY
SFRFHVVVKVYNRQTVQVSLMLNTWPVISAFANDPDVTREAAATSSVLLPLDPGDRVSLRLRRG
NLLGGWKYSSFSGFLIFPL

Signal peptide:

amino acids 1-32

164/270

FIGURE 163

GCTGTTTCTCTCGCGCCACCACTGGCCGCCGGCCGCAGCTCCAGGTGTCCTAGCCGCCCAGC
CTCGACGCCGTCCCGGGACCCCTGTGCTCTGCGCGAAGCCCTGGCCCCGGGGGCCGGGGCAT
GGGCCAGGGGCGCGGGGTGAAGCGGCTTCCCGCGGGGCCGTGACTGGGCGGGCTTCAGCCAT
GAAGACCCTCATAGCCGCCTACTCCGGGGTCCTGCGCGGCGAGCGTCAGGCCGAGGCTGACC
GGAGCCAGCGCTCTCACGGAGGACCTGCGCTGTGCGCGAGGGGTCTGGGAGATGGGGCACT
GGATCCAGCATCCTCTCCGCCCTCCAGGACCTCTTCTCTGTACCTGGCTCAATAGGTCCAA
GGTGGAAGCAGCTACAGGTCATCTCAGTGCTCCAGTGGGTCTGTCTTCTTGTACTGG
GAGTGGCCTGCAGTGCCATCCTCATGTACATATTCTGCACTGATTGCTGGCTCATCGCTGTG
CTCTACTTCACTTGGCTGGTGTGTTGACTGGAACACACCCAAGAAAGGTGGCAGGAGGTCACA
GTGGGTCCGAACTGGGCTGTGTGGCGCTACTTTGAGACTACTTTCCCATCCAGCTGGTGA
AGACACACAACCTGCTGACCACCAGGAACCTATATCTTTGGATACCACCCCATGGTATCATG
GGCCTGGGTGCCTTCTGCAACTTCAGCACAGAGGCCACAGAAGTGAGCAAGAAGTTCCCAGG
CATACGGCCTTACCTGGCTACACTGGCAGGCAACTTCCGAATGCCTGTGTTGAGGGAGTACC
TGATGTCTGGAGGTATCTGCCCTGTCAGCCGGGACACCATAGACTATTTGCTTTCAAAGAAT
GGGAGTGGCAATGCTATCATCATCGTGGTCCGGGGTGCGGCTGAGTCTCTGAGCTCCATGCC
TGGCAAGAATGCAGTCACCCTGCGGAACCGCAAGGGCTTTGTGAACTGGCCCTGCGTCATG
GAGCTGACCTGGTTCCCATCTACTCCTTTGGAGAGAATGAAGTGTACAAGCAGGTGATCTTC
GAGGAGGGCTCCTGGGGCCGATGGGTCCAGAAGAAGTTCCAGAAATACATTGGTTTCGCCCC
ATGCATCTTCCATGGTTCGAGGCCTCTTCTCCTCCGACACCTGGGGGCTGGTGGCCCTACTCCA
AGCCCATCACCACTGTTGTGGGAGAGCCCATCACCATCCCCAAGCTGGAGCACCCAACCCAG
CAAGACATCGACCTGTACCACACCATGTACATGGAGGCCCTGGTGAAGCTCTTCGACAAGCA
CAAGACCAAGTTCGGCCTCCCGGAGACTGAGGTCTGGAGGTGAACTGAGCCAGCCTTCGGG
GCCAATTCCTGGAGGAACCAGCTGCAAATCACTTTTTTGCTCTGTAAATTTGGAAGTGTCA
TGGGTGTCTGTGGGTATTTAAAAGAAATTATAACAATTTTGCTAAACCAAAAAAAAAAAAA
AA
AAAAAAAAAAAAAAAAAAAA

FIGURE 164

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71184

><subunit 1 of 1, 388 aa, 1 stop

><MW: 43831, pI: 9.64, NX(S/T): 3

MKTLIAAYSGVLRGERQAEADRSQRSHGGPALSREGSGRWGTGSSILSALQDLFSVTWLNRS
KVEKQLQVISVLQWVLSFLVLGVACSAILMYIFCTDCWLI AVL YFTWL VFDWNTPKKGRRS
QWVRNWAVWRYFRDYFPIQLVKTHNLLTTRNYIFGYHPHGIMGLGAF CNFSTEATEVSKKFP
GIRPYLATLAGNFRMPVLR EYLMSSGICPVSRDTIDYLLSKNGSGNAIIIVVGGAESLSSM
PGKNAVTLRNRKGFVKLALRHGADLVPIYSFGENEVYKQVIFEEGSWGRWVQKKFQKYIGFA
PCIFHGRGLFSSDTWGLVPYSKPITTVGEPITIPKLEHPTQQDIDLYHTMYMEALVKLFDK
HKTKFGLPETEVLEVN

Important features of the protein:

Transmembrane domain:

amino acids 76-97

N-glycosylation sites.

amino acids 60-63, 173-176, 228-231

N-myristoylation sites.

amino acids 10-15, 41-46, 84-89, 120-125, 169-174, 229-234, 240-
245, 318-323, 378-383

166/270

FIGURE 165

GGGCGGCGGGATGGGGGCGGGGGCGGCGGGCGCCGCACTCGCTGAGGCCCCGACGCAGGGCCGGGCGGGGCCCA
GGGCCGAGGAGCGCGGCGGCCAGAGCGGGGCGCGGAGGCGACGCCGGGACGCCCCGCGACGAGCAGGTGGCG
GCGGCTGCAGGCTTGTCCAGCCGAAGCCCTGAGGGCAGCTGTTCCCACTGGCTCTGCTGACCTTGTGCCTTGGA
CGGCTGTCCTCAGCGAGGGGCGGTGCACCCGCTCCTGAGCAGCGCCATGGGCCTGCTGGCCTTCTGAAGACCCA
GTTTCGTGCTGCACCTGCTGGTTCGGCTTTGTCTTCGTGGTGAGTGGTCTGGTCATCAACTTCGTCCAGCTGTGCAC
GCTGGCGCTCTGGCCGGTCAGCAAGCAGCTCTACCGCCGCTCAACTGCCGCTCGCCTACTCACTCTGGAGCCA
ACTGGTCATGCTGCTGGAGTGGTGGTCTGCACGGAGTGTACACTGTTACGGACCAGGCCACGGTAGAGCGCTT
TGGGAAGGAGCACGCAGTCATCATCTCAACCACAACCTTCGAGATCGACTTCCTCTGTGGGTGGACCATGTGTGA
GCGCTTCGGAGTGCTGGGGAGCTCCAAGGTCTTCGTAAGAAGGAGCTGCTCTACGTGCCCTCATCGGCTGGAC
GTGGTACTTTCTGGAGATTGTGTTCTGCAAGCGGAAGTGGGAGGAGGACCGGGACACCGTGGTGAAGGGCTGAG
GCGCCTGTCCGACTACCCGAGTACATGTGGTTTCTCCTGTACTGCGAGGGGACGCGCTTCACGGAGACCAAGCA
CCGCGTTAGCATGGAGGTGGCGGCTGCTAAGGGGCTTCCTGTCTCAAGTACCACCTGCTGCCGCGGACCAAGGG
CTTCACCACCCGAGTCAAGTGCCCTCCGGGGGACAGTCGAGCTGTCTATGATGTAACCCTGAACCTCAGAGGAAA
CAAGAACCCGTCCTGTGGGATCCTCTACGGGAAGAAGTACGAGGCGACATGTGCGTGAGGAGATTTCCTCT
GGAAGACATCCCGCTGGATGAAAAAGGAAGCAGCTCAGTGGCTTCATAAACTGTACCAGGAGAAGGACGCGCTCCA
GGAGATATATAATCAGAAGGGCATGTTTCCAGGGGAGCAGTTTAAGCCTGCCCGGAGGCCGTGGACCTCTGAA
CTTCCTGTCTGGGCCACCATTCTCCTGTCTCCCCCTCTTCAGTTTTGTCTTGGGCGTCTTTGCCAQCAGGATCACC
TCTCCTGATCCTGACTTTCTTGGGGTTTGTGGGAGCAGCTTCCTTTGGAGTTCGCAGACTGATAGGAGAATCGCT
TGAACCTGGGAGGTGGAGATTGCAGTGAGCTGAGATGGCATCACTGTACTCCAGCCTAGGCAACAGAGCAAGACT
CAGTCTCAAAAAAAAAAAAAAAAAAAAAAACCAGAAATTCTGGAGTTGAACGTGTGTAGTTACTGACATGAAAA
ATTACATAGAGGCTGAACAGCAGATTGTAGCAGGCAGAAAAAATCAGCAAGCTTGAAGATGGTACCTTGAGATT
TTTCAGGCTAATGAAAAAAGAAATGAAGGAAAATTAACAGCCTCAGAGACCCATGGTGCACCGTCACACAAATCAA
CATATGCATGATGAGAGTCCCAGAAGGAGAGGAGAGAAAGGGTCAGAAAGAAATGGCCACAAGCTGATGAAAAACA
GTAACCTACCCACTCAGGAAGCTCAGTGAACCTCAATGAGGATGAATATCAGAGATCCACACCTAGATATTTCA
AATCAAAGTGTCAAATGACAAAGAATCTTGAAAGCAGCAAGAGATGAGCAACTTATCTTGTTCAAAGGATCTTG
ATCAGATTAACAGCTCATTTCTCCTCAGAAATCATGGGAGCCAGGAGATAGTGGGATGAACACTGTTGAAGGCAA
AACCTTCAACTGTAATTATTGGACTTTTGAGTCTTAGATGGTCCTGACCTCTTTGTCTTCAGGGACAGTTTTTCA
ATTTAATCCCTAATAACAATTAGTCAAGCTTCTTGACCTGTAGGAAGGCCTGTCTTTAGGCCGGGCACAGTGGC
TTACACCTGTAATCCAGCACTTTGGGAGGCCAGACGGGTGGATCATTGGGGTCAGGCTGATCTCAAACCTCCT
GAGTTCAGGTGATCTGCCCGCCTCAGCCTCCCAAAGTGTTGTGATTGCAGGCGTGAGCCACTGCGCCTGGCCGGA
ATTTCTTTTTTAAGGCTGAATGATGGGGGCCAGGCACGATGGCTCACGCCTGTGATCCCAAGTAGCTTGGATTGTA
AACATGCACCACCATGCCTGGCTAATTTTTGTATTTTTAGTAGAGACGTGTTAGCCAGGCTGGTCTCGATCTCCT
GACCTCAAGTGACCACCTGCCTCAGCCTCCCAAAGTACTGGGATTACAGGCGTGAGCCACTGTGCCTGGCCTTGA
GCATCTTGTGATGTGCTTATTGGCCATTTGTATATCTTCTATCTTTTGGGGAATGTCTGTTCAAGTCCTTTG
CCTTTTTAAATTTTTATTATTTATTTATTTATTTTGTAGACAGGGTCTTGTTCGTGTGCCAGGCTGGAGTA
CAGTGGCACAGTCTTGGCTCACTGCAGCCTCGACCTCCTGGGCTGCAGTGATCCTCCACCTCAGCCTCCCTTGT
AGCTGTATTTTTTTGTATTTTGTATTTTGTAGCTGTAGTTTTTGTATTTTTTGTGGAGACAGCATTTACCATGA
TGCCCAGGCTGGTCTTGAACCTCTGAGCTCAAGTGATCTGCCTGCTTCAGCCTCCCAAAGTGCTGGGATTACAGA
CATGAGCCACTGCACCTGGCAAACTCCCAAATTCACACACACACAAAAAACCACTGATTCAAATGGGCA
GAGGGGCCGGTGTGGCCCCAACTACCAGGGAGACTGAAGTGGGAGGATCGCTTGGGCATGAGAAGTCGAGGCTG
CAGTGAGTCGAGGTTGTGCGACTGCATTCCAGCCTGGACAACAGAGTGAGACCCTGTCTC

167/270

FIGURE 166

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71213
><subunit 1 of 1, 368 aa, 1 stop
><MW: 42550, pI: 9.11, NX(S/T): 1
MGLLAFLKTQFVLHLLVGFVVFVVSGLVINQVQLCTLALWPVSKQLYRRLNCRLAYSLWSQLV
MLLEWWSCTECTLFTDQATVERFGKEHAVIILNHNFEIDFLCGWTMCERFGVLGSSKVLAKK
ELLYVPLIGWTWYFLEIVFCKRKWEEDRDTVVEGLRRLSDYPEYMWFLLYCEGTRFTETKHR
VSMEVAAAKGLPVLKYHLLPRTKGFTTAVKCLRGTVAAVYDVTNLNFRGNKNPSLLGILYGKK
YEADMCVRRFPLEDIPLDEKEAAQWLHKLYQEKDALQEIYNQKGMFPGEQFKPARRPWTLN
FLSWATILLSPLFSFVLGVFASGSPLLILTLFLGVGAASFGVRRLLIGESLEPGRWRLQ

Important features of the protein:

Signal peptide:

amino acids 1-25

Transmembrane domains:

amino acids 307-323, 335-352

Tyrosine kinase phosphorylation sites.

amino acids 160-168, 161-169

168/270

FIGURE 167

GATATTCTTTATTTTAAAGAATCTGAAGTACTATGCATCACTCCCTCCAATGTCCTGGGGCA
GCCACCAGGCATATTCATCTTTGTGTGTGTTTTCTTTTGCTTTAGCACTGGGGCACTTCTT
GCTTATTTCTTTGGTAGGAAAGGGGCTCAGTTTGTCTTGTGGGGTTGGTGGCAGGCAGGCCG
GCTTACGCCTGATACGGCCCTGGGTTAGAAGGGAAGGGAAGATAAACTTTTATACAAATGGG
GATAGCTGGGGTCTGAGACCTGCTTCCTCAGTAAAATTCTGCGGATCTGCCTATACCTTCTT
TTCTCTAACCTGGCATAACCCTGCTTAAAGCCTCTCAGGGCTTCTCTCTGTTCTTAGGATCAA
AGTATTTAGAGCTACAAGAGCCCTCATGGTCTGGCCCCTGCCCCCTGGCCAGCTTCATTGT
ACATGTGGTGTTCTCTTGTCTGTTCTGTAATGTGGTATGCCATGGGGTCTTTGCACAAGCCT
TTCCTCTTTGGCTGGACACTGTTCCCTGCCCCCCCCATACTCTTCTACTTAATATGTAGTC
ATCCTGCAGATTTCAATTCTAACATCATTTTCTCCAGGGATCCTGGCCTGACAGAATCTCAT
CTTGTTTAATGCTCTCATAAGACCACTTGTTCCTTTTGCAGCACTTGCCACTCAGTTGTA
TCTTTATGTGCGTTTGTGGTTGTATGGGTGTGTCTGTTCCCCAGAATGCCAGCTCTGAGC
TGCGTGAGGGTCAAGGGCATTGCTGTGCCTGCCAGGTATAGTGCCTACATGTGGTGGGTGCT
CATGTTTTAGAGACTAAATGGAGGAGGAGATGAGGAAAAGATTGAAATCTCTCAGTTCACCA
GATGGTGTAGGGCCCAGCATTGTAAATTCACACGTTGACTGTGCTTGTGAATTATCTGGGGA
TGCAGGTCCTGATTCAGTAGGCCCAGGTTGGGCATCTCTAACAACTCCACGTGATGCTGA
TGCTGGTCCTATGAACTATACTAAATAGTAAGAATCTATGGAGCCAGGCTGGGCATGGTGGC
TCACACCTATGATCCCAGCACTTTGGGAGGCTGAGGCAGGCTGATCACCTGGAGTCAGGATT
TCAAGACTAGCCTGGCCAACATGGTGGAACCCCATCTGTACTAAAAATACACAAATTAGCTG
GGCATGGTGGCACATGCCTGTAGTCCCAGCTACTTGGGAGGCTGAAGCAAGAGAATCGCTTG
AACCTGGGAGGCGGAGGTTGCAGTGAGCCGAGATCAGGCCACTGTATTCCAACCAGGGTGAC
AGAGTGAGACTCTATGTCCAAAAAAAAAAAAA

FIGURE 168

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71234
><subunit 1 of 1, 143 aa, 1 stop
><MW: 15624, pI: 9.58, NX(S/T): 0
MHSLQCPGAATRHILCVCF SFALALGHFLLISLVGKGLSLSCGVGGRQAGLRLIRPWVRR
EGKINFYTN GDSWGLRPASSVKFLGSAYTFFSLTWHTLLKASQGFSLFLGSKYLELQEPSWS
GPCPPGQLHCTCGVLLSFL

Important features of the protein:

Signal peptide:

amino acids 1-28

FIGURE 169

GGCTGGACTGGAACCTCCTGGTCCCAAGTGATCCACCCGCCTCAGCCTCCCAAGGTGCTGTGA
TTATAGGTGTAAGCCACCGTGTCTGGCCTCTGAACAACCTTTTTCAGCAACTAAAAAGCCAC
AGGAGTTGAACTGCTAGGATTCTGACTATGCTGTGGTGGCTAGTGCTCCTACTCCTACCTAC
ATTAAATCTGTTTTTTGTTCTCTTGTAAGTAGCCTTTACCTTCCTAACACAGAGGATCTGT
CACTGTGGCTCTGGCCCAAACCTGACCTTCACTCTGGAACGAGAACAGAGGTTTCTACCCAC
ACCGTCCCCTCGAAGCCGGGACAGCCTCACCTTGCTGGCCTCTCGCTGGAGCAGTGCCCTC
ACCAACTGTCTCACGTCTGGAGGCACTGACTCGGGCAGTGCAGGTAGCTGAGCCTCTTGGA
GCTGCGGCTTTCAAGGTGGGCCTTGCCCTGGCCGTAGAAGGGATTGACAAGCCCCGAAGATTT
CATAGGCGATGGCTCCCACTGCCCAGGCATCAGCCTTGCTGTAGTCAATCACTGCCCTGGGG
CCAGGACGGGCCGTGGACACCTGCTCAGAAGCAGTGGGTGAGACATCACGCTGCCCCGCCAT
CTAACCTTTTCATGTCCTGCACATCACCTGATCCATGGGCTAATCTGAACTCTGTCCCAAGG
AAGCCAGAGCTTGAGTGAGCTGTGGCTCAGACCCAGAAGGGGTCTGCTTAGACCACCTGGTT
TATGTGACAGGACTTGCATTCTCCTGGAACATGAGGGAACGCCGGAGGAAAGCAAAGTGGCA
GGGAAGGAACTTGTGCCAAATTATGGGTGAGAAAGATGGAGGTGTTGGGTTATCACAAGGC
ATCGAGTCTCCTGCATTGAGTGGACATGTGGGGGAAGGGCTGCCGATGGCGCATGACACACT
CGGGACTCACCTCTGGGGCCATCAGACAGCCGTTTCCGCCCCGATCCACGTACCAGCTGCTG
AAGGGCAACTGCAGGCCGATGCTCTCATCAGCCAGGCAGCAGCCAAAATCTGCGATCACCAG
CCAGGGGCAGCCGTCTGGGAAGGAGCAAGCAAAGTGACCATTCTCCTCCCCTCCTTCCCTC
TGAGAGGCCCTCCTATGTCCCTACTAAAGCCACCAGCAAGACATAGCTGACAGGGGCTAATG
GCTCAGTGTGTTGGCCCAGGAGGTGAGCAAGGCCTGAGAGCTGATCAGAAGGGCCTGCTGTGCG
AACACGGAAATGCCTCCAGTAAGCACAGGCTGCAAAAATCCCCAGGCAAAGGACTGTGTGGCT
CAATTTAAATCATGTTCTAGTAATTGGAGCTGTCCCCAAGACCAAAGGAGCTAGAGCTTGGT
TCAAATGATCTCCAAGGGCCCTTATACCCAGGAGACTTTGATTTGAATTTGAAACCCCAA
TCCAAACCTAAGAACCAGGTGCATTAAGAATCAGTTATTGCCGGGTGTGGTGGCCTGTAATG
CCAACATTTTGGGAGGCCGAGGCGGGTAGATCACCTGAGGTGAGGAGTTCAAGACCAGCCTG
GCCAACATGGTGAAACCCCTGTCTCTACTAAAAATACAAAAAACTAGCCAGGCATGGTGGT
GTGTGCCTGTATCCCAGCTACTCGGGAGGCTGAGACAGGAGAATTACTTGAACCTGGGAGGT
GAAGGAGGCTGAGACAGGAGAATCACTTCAGCCTGAGCAACACAGCGAGACTCTGTCTCAGA
AAAAATAAAAAAGAATTATGGTTATTTGTAA

FIGURE 170

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71277

><subunit 1 of 1, 109 aa, 1 stop

><MW: 11822, pI: 8.63, NX(S/T): 0

MLWWLVLLLLPTLKSVFCSLVTSLYLPNTEDLSLWLWPKPDLHSGTRTEVSTHTVPSKPGTA
SPCWPLAGAVPSPTVSRLEALTRAVQVAEPLGSCGFQGGPCPGRRRD

Signal peptide:

amino acids 1-15

172/270

FIGURE 171

GCGGGCCCGCGAGTCCGAGACCTGTCCCAGGAGCTCCAGCTCACGTGACCTGTCACTGCCTC
CCGCCGCCTCCTGCCCCGCGCCATGACCCAGCCGGTGCCCCGGCTCTCCGTGCCCCGCCGCGCT
GGCCCTGGGCTCAGCCGCACTGGGCGCCGCTTCGCCACTGGCCTCTTCCTGGGGAGGCGGT
GCCCCCATGGCGAGGCCGGCGAGAGCAGTGCCTGCTTCCCCCGAGGACAGCCGCCTGTGG
CAGTATCTTCTGAGCCGCTCCATGCGGGAGCACCCGGCGCTGCGAAGCCTGAGGCTGCTGAC
CCTGGAGCAGCCGCAGGGGATTCTATGATGACCTGCGAGCAGGCCAGCTCTTGGCCAACC
TGGCGCGGCTCATCCAGGCCAAGAAGGCGCTGGACCTGGGCACCTTCACGGGCTACTCCGCC
CTGGCCCTGGCCCTGGCGCTGCCCCGGACGGGCGCGTGGTGACCTGCGAGGTGGACGCGCA
GCCCCCGGAGCTGGGACGGCCCCCTGTGGAGGCAGGCCGAGGCGGAGCACAAGATCGACCTCC
GGCTGAAGCCCGCCTTGGAGACCCTGGACGAGCTGCTGGCGGCGGGCGAGGCCGGCACCTTC
GACGTGGCCGTGGTGGATGCGGACAAGGAGAACTGCTCCGCCTACTACGAGCGCTGCCTGCA
GCTGCTGCGACCCGGAGGCATCCTCGCCGTCCTCAGAGTCCTGTGGCGCGGGAAGGTGCTGC
AACCTCCGAAAGGGGACGTGGCGGCCGAGTGTGTGCGAAACCTAAACGAACGCATCCGGCGG
GACGTCAGGGTCTACATCAGCCTCCTGCCCCCTGGGCGATGGACTCACCTTGGCCTTCAAGAT
CTAGGGCTGGCCCCCTAGTGAGTGGGCTCGAGGGAGGGTTGCCTGGGAACCCAGGAATTGAC
CCTGAGTTTTTAAATTCGAAAATAAAGTGGGGCTGGGACACAAAAAAAAAAAAAAAAAAAA

FIGURE 172

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71282
><subunit 1 of 1, 262 aa, 1 stop
><MW: 28809, pI: 8.80, NX(S/T): 1
MTQPVPRLSVPAALALGSAALGAATGLFLGRRCPPWRGRREQCLLPEDSRLWQYLLSRS
MREHPALRSRLRLTLEQPQGDSMMTCEQAQLLANLARLIQAKKALDLGTFTGYSALALALAL
PADGRVVTCEVDAQPPPELGRPLWRQAEAEHKIDLRLKPALETLDELLAAGEAGTFDVAVVDA
DKENCSAYYERCLQLLRPGGILAVLRVLWRGKVLQPPKGDVAAECVRNLNERIRRDVRVYIS
LLPLGDGLTLAFKI

Important features of the protein:**Signal peptide:**

amino acids 1-25

Transmembrane domains:

amino acids 8-30, 109-130

N-glycosylation site.

amino acids 190-193

Tyrosine kinase phosphorylation site.

amino acids 238-246

N-myristoylation sites.

amino acids 22-27, 28-33, 110-115, 205-210, 255-260

Amidation sites.

amino acids 31-34, 39-42

174/270

FIGURE 174

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71286

><subunit 1 of 1, 671 aa, 1 stop

><MW: 74317, pI: 7.61, NX(S/T): 0

MPHAFKPGDLVFAKMKGYPHWPARIDDIADGAVKPPPNKYPIFFFGTHETAFLGPKDLFPYD
KCKDKYGKPNKRKGFNEGLWEIQNNPHASYSAPPPVSSSDSEAPEANPADGSDADEDEDRG
VMAVTAVTATAASDRMESDSDSDKSSDNSGLKRKTPALKMSVSKRARKASSDLDQASVSPSE
EENSESSSESEKTSQDFTPEKKA AVRAPRRGPLGGRKKKKAPSASDSDSKADSDGAKPEPV
AMARSASSSSSSSSSSSDSDSVKKPPRGRKPAEKPLPKPRGRKPKPERPPSSSSSDSDSDEV
DRISEWKRRDEARRRELEARRRREQEEELRRLREQEKEEKERRRERADRGEAERGSGGSSGD
ELREDDEPVKKRGRKGRGRGPPSSSDSEPEAELEREAKKSAKKPQSSSTEPARKPGQKEKRV
RPEEKQQAQKPVKVERTKRSEGF SMDRKVEKKKEPSVEEKLQKLHSEIKFALKVDSPDVKRC
LNALEELGTLQVTSQILQKNTDVVATLKKIRRYKANKDVMKAAEVYTRLKSRVLGPKIEAV
QKVNKAGMEKEKAEEKLAGEELAGEEAPQEKAEDKPSTDLSAPVNGEATSQKGESAEDKEHE
EGRDSEEGPRCGSSEDLHDSVREGPDLD RPGSDRQERERARGDSEALDEES

Signal peptide:

amino acids 1-13

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FIGURE 175

GTTGGTTCTCCTGGATCTTCACCTTACCAACTGCAGATCTTGGGACTCATCAGCCTCAATAATTATATTAAATTA
ACACCATTTGAAAGAGAACATTGTTTTTCATCATGAATGCTAATAAAGATGAAAGACTTAAAGCCAGAAGCCAAGA
TTTTACCTTTTTCTGCTTTGATGATGCTAAGCATGACCATGTTGTTTCTTCCAGTCACTGGCACTTTGAAGCA
AAATATTCCAAGACTCAAGCTAACCTACAAAGACTTGCTGCTTTCAAATAGCTGTATTCCCTTTTTGGGTTTCATC
AGAAGGACTGGATTTTCAAACCTCTTCTCTTAGATGAGGAAAGAGGCAGGCTGCTCTTGGGAGCCAAAGACCACAT
CTTTCTACTCAGTCTGGTTGACTTAAACAAAAATTTTAAAGAGATTTATTGGCCTGCTGCAAAGGAACGGGTGGA
ATTATGTAAATTAGCTGGGAAAGATGCCAATACAGAATGTGCAAAATTCATCAGAGTACTTCAGCCCTATAACAA
AACTCACATATATGTGTGTGGAACCTGGAGCATTTTCATCCAATATGTGGGTATATTGATCTTGGAGTCTACAAGGA
GGATATTATATTCAAACCTAGACACACATAATTTGGAGTCTGGCAGACTGAAATGTCCTTTTCGATCCTCAGCAGCC
TTTTGCTTCAGTAATGACAGATGAGTACCTCTACTCTGGAACAGCTTCTGATTTCTTGGCAAAGATACTGCATT
CACTCGATCCCTTGGGCCTACTCATGACCACCTACATCAGAACTGACATTTAGAGCACTACTGGCTCAATGG
AGCAAAATTTATTGGAACCTTTCTTCATACCAGACCTACAATCCAGATGATGATAAAATATATTTCTTCTTTTCG
TGAATCATCTCAAGAAGGCAGTACCTCCGATAAAACCATCTTTCTCGAGTTGGAAGAGTTTGTAAAGATGATGT
AGGAGGACAACGCAGCCTGATAAACAAGTGGACGACTTTTCTTAAGGCCAGACTGATTTGCTCAATTCCTGGAAG
TGATGGGGCAGATACTTACTTTGATGAGCTTCAAGATATTTATTTACTCCCCACAAGAGATGAAAGAAATCCTGT
AGTATATGGAGTCTTTACTACAACAGCTCCATCTTCAAAGGCTCTGCTGTTTGTGTGTATAGCATGGCTGACAT
CAGAGCAGTTTTTAATGGTCCATATGCTCATAAGGAAAGTGACAGACCATCGTTGGGTGCAGTATGATGGGAGAAT
TCCTTATCCACGGCCTGGTACATGTCCAAGCAAACCTATGACCCACTGATTAAGTCCACCCGAGATTTTCCAGA
TGATGTCATCAGTTTTCATAAAGCGGCACCTCTGTGATGTATAAGTCCGTATACCCAGTTGCAGGAGGACCAACGTT
CAAGAGAATCAATGTGGATTACAGACTGACACAGATAGTGGTGGATCATGTCATTGCAGAAGATGGCCAGTACGA
TGTAATGTTTCTTGGAACAGACATTGGAACCTGTCCTCAAAGTTGTCAGCATTTCAAAGGAAAAGTGGAAATATGGA
AGAGGTAGTGCTGGAGGAGTTGCAGATATTCAAGCACTCATCAATCATCTTGAACATGGAATTGTCTCTGAAGCA
GCAACAATTGTACATTGGTTCCCGAGATGGATTAGTTTCACTCTCTCTTGCACAGATGCGACACTTATGGGAAAGC
TTGCGCAGACTGTTGTCTTGGCAGAGACCCCTACTGTGCTGGGATGGAATGCATGCTCTCGATATGCTCCTAC
TTCTAAAAGGAGAGCTAGACGCCAAGATGTAAAATATGGCGACCCCAATCAGCCAGTCTGGGACATCGAAGACAG
CATTAGTCATGAACTGCTGATGAAAAGGTGATTTTTGGCATTGAATTTAACTCAACCTTTCTGGAATGTATACC
TAAATCCCAACAAGCAACTATTAAATGGTATATCCAGAGGTGAGGGGATGAGCATCGAGAGGAGTTGAAGCCCGA
TGAAAGAATCATCAAAACGGAATATGGGCTACTGATTGCAAGTTTGCAGAAGAAGGATTCTGGGATGTATTACTG
CAAAGCCCAGGAGCACACTTTTCATCCACACCATAGTGAAGCTGACTTTGAATGTCATTGAGAATGAACAGATGGA
AAATACCCAGAGGGCAGAGCATGAGGAGGGGCAGGTCAAGGATCTATTGGCTGAGTCACGGTTGAGATACAAAGA
CTACATCCAAATCCTTAGCAGCCCAAACCTTCAGCCTCGACCACTGCGAACAGATGTGGCACAGGGAGAAGCG
GAGACAGAGAAACAAGGGGGGCCCCAAGTGAAGCACATGCAGGAAATGAAGAAGAAACGAAATCGAAGACATCA
CAGAGACCTGGATGAGCTCCCTAGAGCTGTAGCCACGTAGTTTTCTACTTAATTTAAAGAAAAGAATTCCTTACC
TATAAAAACATTGCCTTCTGTTTTGTATATCCCTTATAGTAATTCATAAATGCTTCCCATGGAGTTTGTCTAAGG
CACAAGACAATAATCTGAATAAGACAATATGTGATGAATATAAGAAAAGGGCAAAAATTCATTTGAACAGTTTTT
CCAAGAACAATCTTGCAACAAGCAAGTATAAGAATTATCCTAAAAATAGGGGGTTTACAGTTGTAAATGTTTTA
TGTTTTGAGTTTTTGAATTTATTGTCTATGTAATAGTTGAGCTAAGCAAGCCCCGAATTTGATAGTGATAAGGT
GCTTTATTCCCTCGAATGTCCATTAAGCATGGAATTTACCATGCAGTTGTGCTATGTTCTTATGAACAGATATAT
CATTCCTATTGAGAACCAGCTACCTTGTGGTAGGGAATAAGAGGTGAGACACAAATTAAGACAACCTCCATTATC
AACAGGAACCTTTCTCAGTGAGCCATTCACTCCTGGAGAATGGTATAGGAATTTGGAGAGGTGCATTATTTCTTTC
TGGCCACTGGGGTTAAATTTAGTGTACTACAACATTGATTTACTGAAGGGCACTAATGTTTCCCCCAGGATTTCT
ATTGACTAGTCAGGAGTAACAGGTTACAGAGAGAAGTTGGTGCTTAGTTATGTGTTTTTTAGAGTATATACTAA
GCTCTACAGGGACAGAATGCTTAATAAATACTTTAATAAGATATGGGAAAATATTTAATAAAAACAAGGAAAACA
TAATGATGTATAATGCATCCTGATGGGAAGGCATGCAGATGGGATTTGTTAGAAGACAGAAGGAAAGACAGCCAT
AAATCTGGCTTTGGGGAAAACCTCATATCCCCATGAAAAGGAAGAACAAATCACAAATAAAGTGAGAGTAATGTAA
TGGAGCTCTTTTCACTAGGGTATAAGTAGCTGCCAATTTGTAATTCATCTGTTAAAAAAAATCTAGATTATAACA
AAGTCTAGCAAAATCTGAGGAAACATAAATCTTCTGAAGAATCATAGGAAGAGTAGACATTTTATTTATAACC
AATGATATTTTCAGTATATATTTCTCTCTTTTAAAAAATATTTATCATACTCTGTATATTAATTTCTTTTACTGC
CTTTATTCTCTCTGTATATTTGGATTTTGTGATTATATTTGAGTGAATAGGAGAAAACATATATAACACACAGA
GAATTAAGAAAATGACATTTCTGGGGAGTGGGGATATATATTTGTTGAATAACAGAACGAGTGTAAATTTTAAAC
AACGGAAGGGTTAAATTAACCTTTTGACATCTTCACTCAACCTTTTCTCATTGCTGAGTTAATCTGTTGTAATT
GTAGTATTGTTTTTGAATTTAACAATAAATAAGCCTGCTACATGT

177/270

FIGURE 176

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71883
><subunit 1 of 1, 777 aa, 1 stop
><MW: 89651, pI: 7.97, NX(S/T): 3
MNANKDERLKARSQDFHLFPALMMLSMTMLFLPVTGTLKQNIPLRLKLTyKDLLLSNSCIPFL
GSSEGLDFQTL LLLDEERGRLLLGA KDHI FLLSLVDLNKNFKKIYWPAAKERVELCKLAGKDA
NTECANFIRVLQPYNKTHIYVCGTGAFHPICGYIDLGVYKEDIIFKLDTHNLESGRLKCPFD
PQQPFASVMTDEYLYSGTASDFLGKDTAFTRSLGPTHDHHYIRTDISEHYWLNGAKFIGTFF
IPDTYNPDDDKIYFFFRSSQEGSTSDKTILSRVGRVCKNDVGGQ RSLINKWTTFLKARLIC
SIPGSDGADTYFDELQDIYLLPTRDERNPVYGVFTTTSSIFKGSAVCVYSMADIRAVFNGP
YAHKESADHRWVQYDGRIPYPRPGTCPSKTYDPLIKSTRDFPDDVISFIKRHSVMYKSVYPV
AGGPTFKRINVDYRLTQIVVDHVIAEDGQYDVMFLGTDIGTVLKVVSISKEKWNMEEVVLEE
LQIFKHSSIILNMELSLKQQQLYIGSRDGLVQLSLHRCDTYGKACADCC LARDPYCAWDGNA
CSRYAPTSKRRARRQDVKYGDPITQCWDIEDSISHETADEKVIFGIEFNSTFLECIPKSQQA
TIKWYIQRSGDEHREELKPDERIIKTEYGLLIRSLQKKDSGMY YCKAQEHTFIHTIVKLT LN
VIENEQMENTQRAEHEEGQVKDLLAESRLRYKDYIQILSSPNFSLDQYCEQMWHREKRRQRN
KGGPKWKHMQEMKKKRNRRHHRDLDELPRAVAT

Important features of the protein:**Signal peptide:**

amino acids 1-36

N-glycosylation sites.

amino acids 139-142, 607-610, 724-727

Tyrosine kinase phosphorylation site.

amino acids 571-576

Gram-positive cocci surface proteins 'anchoring' hexapeptide.

amino acids 32-37

178/270

FIGURE 177

CCCTGACCTCCCTGAGCCACACTGAGCTGGAAGCCGCAGAGGTCATCCTGGAGCATGCCACCGCGGGGAGCAGA
CAACCTCCCAGGTAAGCTGGGAGCAAGACCTGAAGCTGTTTCTTCAGGAGCCTGGTGTATTTTCCCCACCCAC
CTCAGCAGTTTCAGCCAGCAGGGACTGATCAGGTGTGTGTCCTGGAGTGGGGAGCAGAAGGCGTGGCTGGCAAGA
GTGGCCTGGAGAAAGAGGTTTCAGCGCTTGACCAGCCGAGCTGCCCGTGACTACAAGATCCAGAACCATGGGCATC
GGGTGAGGTGGGGGGGCACAGGTGTTCATGTGCACCTTCTTGTCTCAGCAAGAAGAGCTGAGAGAGGGGATCTTGG
AGCCATTGAGGGTGTTCATGGAGCTACAGAGGGGAGGGAAAGGTATTTTAAGGTAACAGTGTGGCACAATAGTTAA
GAGCACAGTTTTTGGAGCTAGACCGACATAGGTTCAAATTTCTTCTGTGTGCTTCCTAGTTCTGTAGCCCCAGGT
AAGGGAGTGACTTAACCTCTCTGGACTTCAATTTCTCTCATCACTAAAGTAGGGCCAATAATAGCACCCACCTCAT
AGGGAAGATTAAATGACATAATGTATGTGATGCAACTAGCAAAGTACCAGTCCCATAGTAAGTCATGCCCCACAG
TATTTCCACCCACCCCTGTTCTCTGCCTTCCCAACCAGGTACTGCAACGACTGGAGCAGAGCGGCAGCAGGCTT
CAGAGCGGGAGGCTCCAAGCATAGAACAGAGGTTACAGGAAGTGCGAGAGAGCATCCGCCGGGCACAGGTGAGCC
AGGTGAAGGGGGCTGCCCGGTGGCCCTGCTGCAGGGGGCTGGCTTAGATGTGGAGCGCTGGCTGAAGCCAGCCA
TGACCCAGGCCCAGGATGAGGTGGAGCAGGAGCGGGCGGCTCAGTGAGGCTCGGCTGTCCAGAGGGACCTCTCTC
CAACCGCTGAGGATGCTGAGCTTTCTGACTTTGAGGAATGTGAGGAGACGGGAGAGCTCTTTGAGGAGCCTGCCC
CCCAAGCCCTGGCCACGAGGGCCCTCCCTGCCCCTGCACACGTGGTATTTTCGCTATCAGGCAGGGCGTGAGGATG
AGCTGACAATCACGGAGGGTGAGTGGCTGGAGGTATAGAGGAGGGAGATGCTGACGAATGGGTCAAGGCTCGGA
ACCAGCACGGCGAGGTAGGCTTTGTCCCTGAGCGATATCTCAACTTCCCGGACCTCTCCCTCCAGAGAGCAGCC
AAGACAGTGACAATCCCTGCGGGGCAGAGCCACAGCATTCTGGCACAGGCCCTGTACAGCTACACCGGACAGA
GTGCAGAGGAGCTGAGCTTCCCTGAGGGGGCACTCATCCGTCTGCTGCCCCGGGCCCAAGATGGAGTAGATGACG
GCTTCTGGAGGGGAGAATTTGGGGGGCCGTGTTGGGGTCTTCCCTCCCTGCTGGTGGGAAGAGCTGCTTGGCCCCC
CAGGGCCACCTGAACCTCTCTGACCCTGAACAGATGCTGCCGTCCCCTTCTCTCTCCAGCTTCTCCCCACCTGCAC
CTACCTCTGTGTTGGATGGGCCCCCTGCACCTGTCTGCTGGGGACAAAGCCCTGGACTTCCCTGGGTTCTTGG
ACATGATGGCACCTCGACTCAGGCCGATGCGTCCACCACCTCCCCCGCCGGCTAAAGCCCCGGATCCTGGCCACC
CAGATCCCCTCACCTGAAGGCCAGGGAAGCCTTGACCCCCAGTGTGCTGTCTGCTATCTTCAAGCTGTGAGATGAG
CCACACCATCAATGATCCAGAGCAACACAGCCAAAAGCTGGAATCGCCCTTATTTCCACCCCTCACCTCCAAGGCT
GGAAACTTGCCCTTCCCATTTCTAGAGCTGGAACCCACTCCTTTTTTTTCCCATTTGTTCTATCATCTCTAGGACC
GGAACCTACTACCTTCTCTTCTGTCTATGACCCTATCTAGGGTGGTGAAATGCCTGAAATCTCTGGGGCTGGAACCC
ATCCATCAAGGTCTCTAGTAGTTCTGGCCACCTCTTTCCCCACCTGGCTCCATGACCCACCCCACTCTGGATG
CCAGGGTCACTGGGGTGGGCTGGGGAGAGGAACAGGCCTTGGGAATCAGGAGCTGGAGCCAGGATGCGAAGCAG
CTGTAATGGTCTGAGCGGATTTATTGACAATGAATAAAGGGCACGAAGGCCAGGCCAGGGCCTGGGCTCTTGTG
CTAAGAGGGCAGGGGGCTACGGTGCTATTGCTTTAGGGGCCACCACGGGCAGGGGCTGCTCCCAGCTGCCAC
GCTCTATCATATGGAGCGAGGTGTTGGGGAAGGCGGGGCAGGCAGCCTGTTGCAGGCAGGGGAAGGAGAAGAGAC
TGAGGGGCTGTGACCTCTCCTGAGGCCCCAGCCTGAGACTGTGCAACTCCAGGTGGAAGTAGAGCTGGTCCCTC
AGCTGGGGGGCAGTGCTGTCCAGTGGAGGGGAGGGCTTTACGCCCCACCCACCCCTGGCCCTGCCAGCTGGTAG
TCCATCAGCACAAATGAAGGAGACTTGGAGAAGAGGAAGAATAACACTGTTGCTTCTGTTCAAGCTGTGTCCAGC
TTTTCCCTGGGGCTCCAGGACCTTCCCTACCTCCACCACCAACCAAGGGATTTATAGCAAAGGCTAAGCCTGC
AGTTTACTCTGGGGGTTGAGGAGCCGAAAGGCTTAAATAGTTTAAAGTAGGTGATGGGAAGATGAGATTACCTCA
TTTAGGGCTCAGGCAGACTCACCTCACATACTCCCTGCTCCCTGTGGTAGAGACACCTGAGAGAAAGGGGAGGGG
TCAACAATGAGAGACCAGGAGTAGGTCTTATCAGTGCCCCCAGAGTAGAGAGCAATAAGAGCCCCAGCCAGTGC
AGTCCCGGCTGTGTTTCTTCTACCTGGTGATCAGAAGTGTCTGGTTTGCTTGGCTGCCCATTTGCCCTCTTGAAGTGG
GCAGCCCTGGGCTTGGGCCCCCTCCCTCCGGCCCTCAGTGTGGCTCTGCAGAAGCTCTGGGGTTCCCTTCAAGTG
CACGAGGGGTTAGGCTGCTGTCCCTGAGTCTCCATTTCTGTACTGGGGGGCTGGCTAGGACCTGGGGCTGTGGCC
TCTCAGGGGCGAGCCTCTCCATGGCAGGCATCCCTGCCTTGGGCTGCCCTCCCCCAGACCCCTGACCACCCCTG
GGTCTGTCCCCCACCAGAGCCCCAGTCTCTGTGTGGGGGAGCCATCACGGTGTTCGTGCACTCCATAGCGCT
TCTCAATGTGTGTACCCGGAACCTGGGAGGGGAGGGAACACTGGGGTTTAGGACCACAACCTCAGAGGCTGCTTG
GCCCTCCCCCTGACCAGGGACATCCTGAGTTTGGTGGCTACTTCCCTCTGGCCTAAGGTAGGGGAGGCCTTCTC
AGATTGTGGGGCACATTGTGTAGCCTGACTTCTGCTGGAGCTCCAGTCCAGGAGGAAAGAGCCAAGGCCACTT
TTGGGATCAGGTGCTGATCACTGGGCCCCCTACCTCAGCCCCCTTTCCCTGGAGCAGCTGCCCCACCTGCCCA
CAGAGAACACAGTGGTCTCCCTGTCCGGGGGGCGCTTTTTCTTCTTGGAGCGTCCCTGACGGACAAGTGGAG
GCCTCTGTGCTGGGCTGCAATGGATGCAAGGGGCTGCAGAGCCCAGGTGCACTGTGTGATGATGGGAGGGGGCTC
CGTCTGCAGGCTGGAGGTGGCATCCACACTGGACAGCAGGAGGAGGGAGTGAGGGTAACATTGCCATTTCCCT
TCATGTTTTGTTTCTTACGTTCTTTTCAGCATGCTCTTAAACCCCAAGCCCCAATTTCCCAAGCCCCATTT
TTTCTTGTCTTTATCTAATAAACTCAATATTAAG

179/270

FIGURE 178

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73401

><subunit 1 of 1, 370 aa, 1 stop

><MW: 40685, pI: 4.53, NX(S/T): 0

MQLAKYQSHSKSCPTVFPPTPVLCLPNQVLQRLEQRRQQASEREAPSIEQRLQEVRESIRRA
QVSQVKGAARLALLQGAGLDVERWLKPAMTQAQDEVEQERRLSEARLSQRDLSPTAEDAELS
DFEECEETGELFEPPAPQALATRALPCPAHVVFYQAGREDELTITEGEWLEVIEEGDADEW
VKARNQHGEVGFVPERYLNFPDLSLPESQSDNPGAEPTAFLAQALYSYTGQSAEELSFP
EGALIRLLPRAQDGVDDGFWRGEFGGRVGVFPSLLVEELLGPPGPPELSDPEQMLPSPSPPS
FSPPAPTSVLDGPPAPVLPGDKALDFPGFLDMMAPRLRPMRPPPPPPAKAPDPGHDPDPLT

180/270

FIGURE 179A

CACAGGGAGACCCACAGACACATATGCACGAGAGAGACAGAGGAGGAAAGAGACAGAGACAAAGGCACAGCGGAA
GAAGGCAGAGACAGGGCAGGCACAGAAGCGGCCAGACAGAGTCTTACAGAGGGAGAGGCCAGAGAAGCTGCAGA
AGACACAGGCAGGGAGAGACAAAGATCCAGGAAAGGAGGGCTCAGGAGGAGAGTTTGGAGAAGCCAGACCCCTGG
GCACCTCTCCCAAGCCCAAGGACTAAGTTTTCTCCATTTCTTTAACGGTCTCTCAGCCCTTCTGAAAACCTTTGCC
TCTGACCTTGGCAGGAGTCCAAGCCCCCAGGCTACAGAGAGGAGCTTTCCAAAGCTAGGGTGTGGAGGACTTGGT
GCCCTAGACGGCTCAGTCCCTCCCAGCTGCAGTACCAGTGCCATGTCTCCAGACAGGCTCGCATCCCCGGGAGGGG
CTTGGCAGGGCGCTGGCTGTGGGGAGCCCCAACCTTGCCCTCTGCTCCCCATTGTGCCGTCTCTCTGGCTGGTGTG
GCTGCTTCTGCTACTGCTGGCCTCTCTCTGCCCCTCAGCCCCGGCTGGCCAGCCCCCTCCCCGGGAGGAGGAGAT
CGTGTTTCCAGAGAAGCTCAACGGCAGCGTCTCTGCTGGCTCGGGCGCCCCTGCCAGGCTGTTGTGCCGCTTGA
GGCCTTTGGGGAGACGCTGCTACTAGAGCTGGAGCAGGACTCCGGTGTGCAGGTGAGGGGCTGCAGTGCAGT
CCTGGGCCAGGCGCTGAGCTGCTGGGTGGAGCAGAGCTGGCACTACCTGACTGTCACCATCAATGGAGATCC
GGAGTCGGTGGCATCTCTGCACTGGGATGGGGAGCCCTGTTAGGCGTGTTTACAATATCGGGGGCTGAACCTCCA
CCTCCAGCCCCCTGGAGGGAGGCACCCCTAACTCTGCTGGGGGACCTGGGGCTCACATCTTACGCCGGAAGAGTCC
TGCCAGCGGTCAAGGTCCCATGTGCAACGTCAAGGCTCCTCTTGGAAGCCCCAGCCCCAGACCCCGAAGAGCCAA
GCGCTTTGCTTCACTGAGTAGATTTGTGGAGACACTGGTGGTGGCAGATGACAAGATGGCCGCATTCCACGGTGC
GGGGCTAAAGCGCTACCTGCTAACAGTGATGGCAGCAGCAGCCAAGGCCTTCAAGCACCCAAGCATCCGCAATCC
TGTCAGCTTGGTGGTGACTCGGCTAGTGATCCTGGGGTCAGGCGAGGAGGGGGCCCCAAGTGGGGCCAGTGCTGC
CCAGACCCCTGCGCAGCTTCTGTGCCTGGCAGCGGGGCCCTCAACACCCCTGAGGACTCGGGCCCTGACCATTGTA
CACAGCCATTCTGTTTACCCGTCAGGACCTGTGTGGAGTCTCCACTTGCAGACACGCTGGGTATGGCTGATGTGGG
CACCGTCTGTGACCCGGCTCGGAGCTGTGCCATTGTGGAGGATGATGGGCTCCAGTCAGCCTTCACTGCTGCTCA
TGAATGGGTGATGCTTCAACATGCTCCATGACAACCTCAAGCCATGCATCAGTTTGAATGGGCCTTTGAGCAC
TCTCGCCATGTATCGGCCCTGTGATGGCTCATGTGGATCTTGAGGAGCCCTGGTCCCCCTGCAGTGCCTCGCT
CATCATGACTTCTTGGACAATGGCTATGGGCATGTCTCTTAGACAACACAGAGGCTCCATTGCATCTGCTCGTGT
GACTTTCCCTGGCAAGGACTATGATGCTGACCGCCAGTGCCAGCTGACCTTCGGGCCCCGACTCACGCCATTGTCC
ACAGCTGCCGCCGCCCTGTGCTGCCCTCTGGTGCTCTGGCCACCTCAATGGCCATGCCATGTGCCAGACCAAACA
CTCGCCCTGGGCCGATGGCACACCCCTGCGGGCCCCGCACAGGCCTGCATGGGTGGTTCGCTGCCCTCCACATGGACCA
GCTCCAGGACTTCAATATTCCACAGGCTGGTGGCTGGGGTCTTGGGGACCATGGGGTGACTGCTCTCGGACCTG
TGGGGGTGGTGTCCAGTTCTCCTCCCAGAGACTGCACGAGGCCTGTCCCCCGGAATGGTGGCAAGTACTGTGAGGG
CCGCCGTACCCGCTTCCGCTCCTGCAACACTGAGGACTGCCCAACTGGCTCAGCCCTGACCTTCCGCGAGGAGCA
GTGTGCTGCCCTACAACCACCGCACCGACCTCTTCAAGAGCTTCCCAGGGCCCATGGACTGGGTTCTCTGCTACAC
AGGCGTGGCCCCCAGGACCAAGTGCAAACTCACCTGCCAGGCCCGGGCACTGGGCTACTACTATGTGCTGGAGCC
ACGGTGGTGTAGATGGGACCCCTGTCTCCCCGACAGCTCCTCGGTCTGTGTCAGGGCCGATGCATCCATGTCTGG
CTGTGATCGCATCATATGGCTCCAAGAAGAAGTTTGACAAGTGATGTGTCGCGAGGGGACGGTTCTGGTTGACG
CAAGCAGTCAGGCTCCTTCAGGAAATTAGGTACGGATAACAACATGTGGTCACTATCCCCGGGGGGCCACCCA
CATTTCTTGTCCGGCAGCAGGGAAACCCTGGCCACCGGAGCATCTACTTGGCCCTGAAGCTGCCAGATGGCTCCTA
TGCCCTCAATGGTGAATACACGCTGATGCCCTCCCCACAGATGTGGTACTGCCTGGGGCAGTCAGCTTGCCTA
CAGCGGGGCCACTGCAGCCTCAGAGACACTGTAGGCCATGGGCCACTGGCCAGCCTTTGACACTGCAAGTCCT
AGTGGCTGGCAACCCCAAGGACACACGCTCCGATACAGCTTCTTCTGTGCCCGGCCGACCCCTTCAACGCCACG
CCCCACTCCCCAGGACTGGCTGCACCGAAGAGCACAGATTCTGGAGATCCTTCGGCGGCGCCCCCTGGGCGGGCAG
GAAATAACCTCACTATCCCCGGCTGCCCTTTCTGGGCACCGGGGCCTCGGACTTAGCTGGGAGAAAGAGAGAGCTT
CTGTTGCTGCCCTCATGCTAAGACTCAGTGGGGAGGGGCTGTGGGCGTGAGACCTGCCCTCCTCTCTGCCCTAAT
GCGCAGGCTGGCCCTGCCCTGGTTTCTGCCCTGGGAGGCAGTGATGGGTTAGTGGATGGAAGGGGCTGACAGAC
AGCCCTCCATTAACCTGCCCTCTGCCCTGCGGTCACAGGAGGGAGGGGGAAGGCAGGAGGGGCTGGGCCC
CAGTTGTATTATTTAGTATTTATTACTTTTATTTAGCACACAGGGAAGGGGACAGGACTAGGGCTCTGGGGAA
CCTGACCCCTGACCCCTCATAGCCCTCACCTTGGGGCTAGGAAATCCAGGGTGGTGGTATAGGTATAAGTGGTG
TGTGTATGCGTGTGTGTGTGTGTGAAAATGTGTGTGTGCTTATGTATGAGGTACAACCTGTTCTGCTTTCTCT
TTCTTGAATTTTATTTTTTTGGGAAAAGAAAAGTCAAGGGTAGGGTGGGCCTTCAGGGAGTGAGGGATTATCTTTT
TTTTTTTTTCTTTCTTCTTTCTTTTTTTTTTTTGTAGACAGAATCTCGCTCTGTGCCCCAGGCTGGAGTGCAATG
GCACAATCTCGGCTCACTGCATCCTCCGCTCCCGGGTTCAAGTGATTCTCATGCCCTCAGCCTCCTGAGTAGCTG
GGATTACAGGCTCCTGCCACCACGCCAGCTAATTTTTGTTTTGTTTTGTTTTGGAGACAGAGTCTCGCTATTGTC
ACCAGGGCTGGAATGATTTTCACTCACTGCAACCTTCGCCACCTGGGTTCCAGCAATTTCTCTGCCCTCAGCCTCC
CGAGTAGCTGAGATTATAGGCACCTACCACCACGCCCGGCTAATTTTTGTATTTTTTAGTAGAGACGGGGTTTAC
CATGTTGGCCAGGCTGGTCTCGAATCCTGACCTTAGGTGATCCACTCGCCTTATCTCCCCAAGTGCTGGGATT
ACAGGCGTGAGCCACCGCTGGCCACGCCCAACTAATTTTTGATTTTTAGTAGAGACAGGGTTTCAACATGT
TGGCCAGGCTGCTCTTGAACCTCTGACCTCAGGTAATCGACCTGCCCTCGGCCCTCCCAAGTGCTGGGATTACAGG
TGTGAGCCACCACGCCCGGTACATATTTTTTAAATTGAATTCTACTATTTATGTGATCCTTTTGGAGTCAGACAG

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FIGURE 179B

ATGTGGTTGCATCCTAACTCCATGTCTCTGAGCATTAGATTTCTCATTTGCCAATAATAATACCTCCCTTAGAAG
TTTGTGTTGAGGATTAAATAATGTAAATAAAGAACTAGCATAACACTCAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
AAGGAAA

FIGURE 180

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73492
><subunit 1 of 1, 837 aa, 1 stop
><MW: 90167, pI: 8.39, NX(S/T): 1
MSQTGSHPGRGLAGRWLWGAQPCLLLPIVPLSWLVWLLLLLLASLLPSARLASPLPREEEIV
FPEKLNGSVLPGSGAPARLLCRLQAFGETLLLELEQDSGVQVEGLTVQYLGQAPELLGGAEP
GTYLGTGTINGDPESVASLHWDGGALLGVLQYRGAEHLQPLEGGTPNSAGGPGAHILRRKSP
ASGQGPMCNCVKAPLGSPSPRRRAKRFASLSRFVETLVVADDKMAAFHGAGLKRYLLTVMAA
AAKAFKHPSIRNPVSLVVTRLVILSGGEEGPQVGPSAAQTLRSFCAWQRLNTPEDSGPDHF
DTAILFTRQDLCGVSTCDTLGMADVGTVCDPARSCAIVEDDGLQSAFTAAHELGHVFNMLHD
NSKPCISLNGPLSTSRHVMAPVMAHVDPEEPWSPCSARFITDFLDNGYGHCLLDKPEAPLHL
PVTFFPGKDYDADRQCQLTFGPDSRHCPQLPPPCAALWCSGHLNGHAMCQTKHSPWADGTPCG
PAQACMGGRCCLHMDQLQDFNIPQAGGWGPWGPWGDCSRTC GGGVQFSSRDCTRVPVPRNGGKY
CEGRRTFRSCNTEDCPTGSALTFREEQCAAYNHRTDLFKSFPGPMDWVPRYTGVAPQDQCK
LTCQARALGYYYVLEPRVVDGTPCSPDSSVCVQGRCIHAGCDRIIGSKKKFDKCMVCGGDG
SGCSKQSGSFRKFRYGYNVVTIPAGATHILVRQQGNPGHRSIYLALKLPDGSYALNGEYTL
MPSPTDVVLPGAVSLRYSGATAASETLSGHGPLAQPLTLQVLVAGNPQDTRLRYSFFVPRPT
PSTPRPTPDWLHRRRAQILEILRRRPWAGRK
```

Important features of the protein:**Signal peptide:**

amino acids 1-48

N-glycosylation site.

amino acids 68-71

Glycosaminoglycan attachment site

amino acids 188-191, 772-775

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 182-185

Tyrosine kinase phosphorylation site.

amino acids 730-736

N-myristoylation sites.

amino acids 5-10, 19-24, 121-126, 125-130, 130-135, 147-152, 167-172, 168-173, 174-179, 323-328, 352-357, 539-544, 555-560, 577-582, 679-684, 682-687, 763-768

Amidation sites.

amino acids 560-563, 834-837

Leucine zipper pattern.

amino acids 17-38, 24-45

Neutral zinc metalloproteinases, zinc-binding region signature.

amino acids 358-367

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FIGURE 181

CAGCAGTGGTCTCTCAGTCCTCTCAAAGCAAGGAAAGAGTACTGTGTGCTGAGAGACCATGG
CAAAGAATCCTCCAGAGAATTGTGAAGACTGTCACATTCTAAATGCAGAAGCTTTTAAATCC
AAGAAAATATGTAAATCACTTAAGATTTGTGGACTGGTGTGTTGGTATCCTGGCCCTAACTCT
AATTGTCCTGTTTTGGGGGAGCAAGCACTTCTGGCCGGAGGTACCCAAAAAGCCTATGACA
TGGAGCACACTTTCTACAGCAATGGAGAGAAGAAGAAGATTTACATGGAAATTGATCCTGTG
ACCAGAACTGAAATATTCAGAAGCGGAAATGGCACTGATGAAACATTGGAAGTGCACGACTT
TAAAAACGGATACACTGGCATCTACTTCGTGGGTCTTCAAAAATGTTTTATCAAACTCAGA
TTAAAGTGATTCTGAATTTTCTGAACCAGAAGAGGAAATAGATGAGAATGAAGAAATTACC
ACAACCTTTCTTTGAACAGTCAGTGATTTGGGTCCCAGCAGAAAAGCCTATTGAAAACCGAGA
TTTTCTTAAAAATTCCAAAATTCTGGAGATTTGTGATAACGTGACCATGTATTGGATCAATC
CCACTCTAATATCAGTTTCTGAGTTACAAGACTTTGAGGAGGAGGGAGAAGATCTTCACTTT
CCTGCCAACGAAAAAAAAGGGATTGAACAAAATGAACAGTGGGTGGTCCCTCAAGTGAAAGT
AGAGAAGACCCGTACGCCAGACAAGCAAGTGAGGAAGAACTTCCAATAAATGACTATACTG
AAAATGGAATAGAATTTGATCCCATGCTGGATGAGAGAGGTTATTGTTGTATTTACTGCCGT
CGAGGCAACCGCTATTGCCGCCGCGTCTGTGAACCTTTACTAGGCTACTACCCATATCCATA
CTGCTACCAAGGAGGACGAGTCATCTGTGTCATCATGCCTTGTAAGTGGTGGGTGGCCC
GCATGCTGGGGAGGGTCTTAATAGGAGGTTTGAGCTCAAATGCTTAAACTGCTGGCAACATAT
AATAAATGCATGCTATTCAATGAATTTCTGCCTATGAGGCATCTGGCCCCTGGTAGCCAGCT
CTCCAGAATTACTTGTAGGTAATTCCTCTCTTCATGTTCTAATAAACTTCTACATTATCACC
AAAAAAAAAAAAAAAAAAAA

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FIGURE 182

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73727

><subunit 1 of 1, 317 aa, 1 stop

><MW: 37130, pI: 5.18, NX(S/T): 3

MAKNPPENCEDCHILNAEAFKSKKICKSLKICGLVFGILALTILVLFWGSKHFWPEVPPKAY
DMEHTFYSSNGEKKKIYMEIDPVTRTEIFRSGNGTDETLVHDFKNGYTGIFYVGLQKCFIKT
QIKVIPEFSEPEEEIDENEEITTTFFEQSVIWPVPAEKPIENRDFLKNKILEICDNVTMYWI
NPTLISVSELQDFEEEGEDLHFPANEKKGIEQNEQWVVPQVKVEKTRHARQASEEELPINDY
TENGIEFDPMLEDERGYCCIIYCRRGNRYCRRVCEPLLGYYPYPYCYQGGRVICRVIMPCNWWV
ARMLGRV

Important features of the protein:

Signal peptide:

amino acids 1-40

Transmembrane domain:

amino acids 25-47 (type II)

N-glycosylation sites.

amino acids 94-97, 180-183

Glycosaminoglycan attachment sites.

amino acids 92-95, 70-73, 85-88, 133-136, 148-151, 192-195, 239-242

N-myristoylation sites.

amino acids 33-38, 95-100, 116-121, 215-220, 272-277

Microbodies C-terminal targeting signal.

amino acids 315-317

Cytochrome c family heme-binding site signatur .

amino acids 9-14

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FIGURE 183

GCGGAACTGGCTCCGGCTGGCACCTGAGGAGCGGCGTGACCCCGAGGGCCCAGGGAGCTGCC
CGGCTGGCCTAGGCAGGCAGCCGCACCAATGGCCAGCACGGCCGTGCAGCTTCTGGGCTTCCT
GCTCAGCTTCCTGGGCATGGTGGGCACGTTGATCACCACCATCCTGCCGCACTGGCGGAGGA
CAGCGCACGTGGGCACCAACATCCTCACGGCCGTGTCCTACCTGAAAGGGCTCTGGATGGAG
TGTGTGTGGCACAGCACAGGCATCTACCAGTGCCAGATCTACCGATCCCTGCTGGCGCTGCC
CCAAGACCTCCAGGCTGCCCCGCGCCCTCATGGTCATCTCCTGCCTGCTCTCGGGCATAGCCT
GCGCCTGCGCCGTCATCGGGATGAAGTGCACGCGCTGCGCCAAGGGCACACCCGCCAAGACC
ACCTTTGCCATCCTCGGCGGCACCCTCTTCATCCTGGCCGGCCCTCCTGTGCATGGTGGCCGT
CTCCTGGACCACCAACGACGTGGTGCAGAACTTCTACAACCCGCTGCTGCCCAGCGGCATGA
AGTTTGAGATTGGCCAGGCCCTGTACCTGGGCTTCATCTCCTCGTCCCTCTCGCTCATTGGT
GGCACCTTGCTTTGCCTGTCCTGCCAGGACGAGGCACCCTACAGGCCCTACCAGGCCCGCC
CAGGGCCACCACGACCACTGCAAACACCGCACCTGCCTACCAGCCACCAGCTGCCTACAAAG
ACAATCGGGCCCCCTCAGTGACCTCGGCCACGCACAGCGGGTACAGGCTGAACGACTACGTG
TGAGTCCCCACAGCCTGCTTCTCCCCTGGGCTGCTGTGGGCTGGGTCCCCGGCGGGACTGTC
AATGGAGGCAGGGGTTCCAGCACAAAGTTTACTTCTGGGCAATTTTTGTATCCAAGGAAATA
ATGTGAATGCGAGGAAATGTCCTTTAGAGCACAGGGACAGAGGGGGAAATAAGAGGAGGAGAA
AGCTCTCTATACCAAAGACTGAAAAAAAAAATCCTGTCTGTTTTTGTATTTATTATATATAT
TTATGTGGGTGATTTGATAACAAGTTTAATAAAGTGACTTGGGAGTTTGGTCAGTGGGGT
TGTTTTGTGATCCAGGAATAAACCTTGCGGATGTGGCTGTTTATGAAAAAAAAAAAAA

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FIGURE 184

MASTAVQLLGFLLSFLGMVGTLITLPHWRRTAHVGTNILTAVSYLKGLWMECVWHSTGIY
QCQIYRSLLALPQDLQAARALMVISCLLSGIACACAVIGMKCTRCAKGTPAKTTFAILGGTL
FILAGLLCMVAVSWTTNDVVQNFYNPLLPSPGMKFEIGQALYLGFISSSLSLIGGTLLCLSCQ
DEAPYRPYQAPPRATTTTANTAPAYQPPAAYKDNRAPSVTSATHSGYRLNDYV

Important features of the protein:

Signal peptide:

amino acids 1-21

Transmembrane domains:

amino acids 82-103, 115-141, 160-182

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FIGURE 185

GAGCTCCCCTCAGGAGCGCGTTAGCTTCACACCTTCGGCAGCAGGAGGGCGGCAGCTTCTCG
CAGGCGGCAGGGCGGGCGGCCAGGATCATGTCACCAACCATGCCAAGTGGTGGCGTTCCCT
CCTGTCCATCCTGGGGCTGGCCGGCTGCATCGCGGCCACCGGGATGGACATGTGGAGCACCC
AGGACCTGTACGACAACCCCGTCACCTCCGTGTTCCAGTACGAAGGGCTCTGGAGGAGCTGC
GTGAGGCAGAGTTCAGGCTTCACCGAATGCAGGCCCTATTTACCATCCTGGGACTTCCAGC
CATGCTGCAGGCAGTGCGAGCCCTGATGATCGTAGGCATCGTCCTGGGTGCCATTGGCCTCC
TGGTATCCATCTTTGCCCTGAAATGCATCCGCATTGGCAGCATGGAGGACTCTGCCAAAGCC
AACATGACACTGACCTCCGGGATCATGTTTATTGTCTCAGGTCTTTGTGCAATTGCTGGAGT
GTCTGTGTTTGCCAACATGCTGGTGAATACTTCTGGATGTCCACAGCTAACATGTACACCG
GCATGGGTGGGATGGTGCAGACTGTTTCAGACCAGGTACACATTTGGTGC GGCTCTGTTCGTG
GGCTGGGTGCGCTGGAGGCCTCACACTAATTGGGGGTGTGATGATGTGCATCGCCTGCCGGGG
CCTGGCACCAGAAGAAACCAACTACAAAGCCGTTTCTTATCATGCCTCAGGCCACAGTGTTG
CCTACAAGCCTGGAGGCTTCAAGGCCAGCACTGGCTTTGGGTCCAACACCAAAAACAAGAAG
ATATACGATGGAGGTGCCCGCACAGAGGACGAGGTACAATCTTATCCTTCCAAGCACGACTA
TGTGTAATGCTCTAAGACCTCTCAGCACGGGCGGAAGAACTCCCGGAGAGCTCACCAAAA
AACAAGGAGATCCCATCTAGATTTCTTCTTGCTTTTGACTCACAGCTGGAAGTTAGAAAAGC
CTCGATTTTCATCTTTGGAGAGGCCAAATGGTCTTAGCCTCAGTCTCTGTCTCTAAATATTCC
ACCATAAAACAGCTGAGTTATTTATGAATTAGAGGCTATAGCTCACATTTTCAATCCTCTAT
TTCTTTTTTTAAATATAACTTTCTACTCTGATGAGAGAATGTGGTTTTAATCTCTCTCTCAC
ATTTTGATGATTTAGACAGACTCCCCCTCTTCTCCTAGTCAATAAACCCATTGATGATCTA
TTTCCCAGCTTATCCCCAAGAAAACCTTTTGAAAGGAAAGAGTAGACCCAAAGATGTTATTTT
CTGCTGTTTGAATTTTGTCTCCCCACCCCAACTTGGCTAGTAATAAACACTTACTGAAGAA
GAAGCAATAAGAGAAAGATATTTGTAATCTCTCCAGCCCATGATCTCGGTTTTCTTACACTG
TGATCTTAAAGTTACCAAACCAAAGTCATTTTCAGTTTGAGGCAACCAAACCTTTCTACTG
CTGTTGACATCTTCTTATTACAGCAACACCATTCTAGGAGTTTCTGAGCTCTCCACTGGAG
TCCTCTTTCTGTGCGGGTCAGAAATTGTCCCTAGATGAATGAGAAAATTATTTTTTTTAAAT
TTAAGTCCTAAATATAGTTAAAATAAATAATGTTTTAGTAAAATGATACACTATCTCTGTGA
AATAGCCTCACCCCTACATGTGGATAGAAGGAAATGAAAAAATAATTGCTTTGACATTGTCT
ATATGGTACTTTGTAAAGTCATGCTTAAGTACAAATTCCATGAAAAGCTCACACCTGTAATC
CTAGCACTTTGGGAGGCTGAGGAGGAAGGATCACTTGAGCCCAGAAGTTCGAGACTAGCCTG
GGCAACATGGAGAAGCCCTGTCTCTACAAAATACAGAGAGAAAAAATCAGCCAGTCATGGTG
GCATACACCTGTAGTCCCAGCATTCGGGGAGGCTGAGGTGGGAGGATCACTTGAGCCCAGGG
AGGTTGGGGCTGCAGTGAGCCATGATCACACCACTGCACTCCAGCCAGGTGACATAGCGAGA
TCCTGTCTAAAAAATAAAAAATAAATAATGGAACACAGCAAGTCCTAGGAAGTAGGTTAAA
ACTAATTCTTTAA

FIGURE 186

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73734

><subunit 1 of 1, 261 aa, 1 stop

><MW: 27856, pI: 8.50, NX(S/T): 1

MSTTTCQVVAFLLSILGLAGCIAATGMDMWSTQDLYDNPVTSVVFQYEGWLWRSCVRQSSGFTE
CRPYFTILGLPAMLQAVRALMIVGIVLGAIGLLVSIFALKCIRIGSMEDSAKANMTLTSGIM
FIVSGLCAIAGVSVFANMLVTNFWMSTANMYTGMGGMVQTVQTRYTFGAALFVGWVAGGLTL
IGGVMMCIACRGLAPEETNYKAVSYHASGHSVAYKPGGFKASTGFGSNTKNKKIYDGGARTE
DEVQSYPSKHDYV

Signal peptide:

amino acids 1-23

Transmembrane domains:

amino acids 81-100, 121-141, 173-194

189/270

FIGURE 187

GGAAAACTGTTCTCTTCTGTGGCACAGAGAACCCTGCTTCAAAGCAGAAGTAGCAGTTCCG
GAGTCCAGCTGGCTAAAACTCATCCCAGAGGATAATGGCAACCCATGCCTTAGAAATCGCTG
GGCTGTTTCTTGGTGGTGGTGGGAATGGTGGGCACAGTGGCTGTCACTGTGCATGCCTCAGTGG
AGAGTGTCCGCCCTTCATTGAAAACAACATCGTGGTTTTTGAAAACCTTCTGGGAAGGACTGTG
GATGAATTGCGTGAGGCAGGCTAACATCAGGATGCAGTGCAAAATCTATGATTCCTTGCTGG
CTCTTTCTCCGGACCTACAGGCAGCCAGAGGACTGATGTGTGCTGCTTCCGTGATGTCCTTC
TTGGCTTTCATGATGGCCATCCTTGGCATGAAATGCACCAGGTGCACGGGGGACAATGAGAA
GGTGAAGGCTCACATTCTGCTGACGGCTGGAATCATCTTCATCATCACGGGCATGGTGGTGC
TCATCCCTGTGAGCTGGGTGCCAATGCCATCATCAGAGATTTCTATAACTCAATAGTGAAT
GTTGCCCAAAAACGTGAGCTTGGAGAAGCTCTCTACTTAGGATGGACCACGGCACTGGTGGCT
GATTGTTGGAGGAGCTCTGTTCTGCTGCGTTTTTTTGTGCAACGAAAAGAGCAGTAGCTACA
GATACTCGATACCTTCCCATCGCACAACCCAAAAAAGTTATCACACCGGAAAGAAGTCACCG
AGCGTCTACTCCAGAAAGTCAGTATGTGTAGTTGTGTATGTTTTTTTAACTTTACTATAAAGC
CATGCAAATGACAAAAATCTATATTACTTTCTCAAATGGACCCCAAAGAAACTTTGATTTA
CTGTTCTTAACTGCCTAATCTTAATTACAGGAAGTGTGCATCAGCTATTTATGATTCTATAA
GCTATTTTCAGCAGAATGAGATATTAACCCAATGCTTTGATTGTTCTAGAAAGTATAGTAAT
TTGTTTTCTAAGGTGGTTCAAGCATCTACTCTTTTATCATTTACTTCAAATGACATTGCT
AAAGACTGCATTATTTTACTACTGTAATTTCTCCACGACATAGCATTATGTACATAGATGAG
TGTAACATTTATATCTCACATAGAGACATGCTTATATGGTTTTATTTAAATGAAATGCCAG
TCCATTACACTGAATAAATAGAACTCAACTATTGCTTTTTCAGGGAAATCATGGATAGGGTTG
AAGAAGGTTACTATTAATTGTTTAAAAACAGCTTAGGGATTAATGTCCTCCATTTATAATGA
AGATTAAAATGAAGGCTTTAATCAGCATTGTAAAGGAAATGAAATGGCTTTCTGATATGCTG
TTTTTTAGCCTAGGAGTTAGAAATCCTAACTTCTTTATCCTCTTCTCCCAGAGGCTTTTTTT
TTCTTGTGTATTAAATTAACATTTTTTAAAACGCAGATATTTTGTCAAGGGGCTTTGCATTCA
AACTGCTTTTCCAGGGCTATACTCAGAAGAAAGATAAAAGTGTGATCTAAGAAAAAGTGATG
GTTTTAGGAAAGTGAAAATATTTTTGTTTTTGTATTTGAAGAAGAATGATGCATTTTGACAA
GAAATCATATATGTATGGATATATTTTAATAAGTATTTGAGTACAGACTTTGAGGTTTCATC
AATATAAATAAAAAGAGCAGAAAAATATGTCTTGGTTTTTCATTTGCTTACCAAAAAACAACA
ACAAAAAAGTTGTCTTTTGAGAACTTCACCTGCTCCTATGTGGGTACCTGAGTCAAAATTG
TCATTTTTGTTCTGTGAAAAATAAATTTCTTCTGTACCATTTCTGTTAGTTTTACTAAA
ATCTGTAAATACTGTATTTTTCTGTTTATTCCAAATTTGATGAACTGACAATCCAATTTGA
AAGTTTGTGTGACGCTGTCTAGCTTAAATGAATGTGTTCTATTTGCTTTATACATTTATA
TTAATAAATTGTACATTTTTCTAATT

FIGURE 188

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73735

><subunit 1 of 1, 225 aa, 1 stop

><MW: 24845, pI: 9.07, NX(S/T): 0

MATHALEIAGLFLGGVGMVGTVAVTVMPPQWRVSAFIENNIVVFENFWEGLWMNCVRQANIRM
QCKIYDSLLALSPDLQAARGLMCAASVMSFLAFMMAILGMKCTRCTGDNEKVKAHILLTAGI
IFIITGMVVLIPVSWVANAIIRDFYNSIVNVAQKRELGEALYLGWTTALVLIVGGALFCCVF
CCNEKSSSYRYSIPSHRTTQKSYHTGKKSPSVYSRSQYV

Signal peptide:

amino acids 1-17

Transmembrane domains:

amino acids 82-101, 118-145, 164-188

191/270

FIGURE 189

TCGCCATGGCCTCTGCCGGAATGCAGATCCTGGGAGTCGTCTTGACACTGCTGGGCTGGGTG
AATGGCCTGGTCTCCTGTGCCCTGCCCATGTGGAAGGTGACCGCTTTCATCGGCAACAGCAT
CGTGGTGGCCCAGGTGGTGTGGGAGGGCCTGTGGATGTCCTGCGTGGTGCAGAGCACCGGCC
AGATGCAGTGCAAGGTGTACGACTCACTGCTGGCGCTGCCACAGGACCTGCAGGCTGCACGT
GCCCTCTGTGTATCGCCCTCCTTGTGGCCCTGTTCCGGCTTGCTGGTCTACCTTGCTGGGGC
CAAGTGTACCACCTGTGTGGAGGAGAAGGATTCCAAGGCCCGCCTGGTGCTCACCTCTGGGA
TTGTCTTTGTATCTCAGGGGTCTTGACGCTAATCCCCGTGTGCTGGACGGCGCATGCCATC
ATCCGGGACTTCTATAACCCCTGGTGGCTGAGGCCCAAAGCGGGAGCTGGGGGCCCTCCCT
CTACTTGGGCTGGGCGGCCTCAGGCCTTTTGTGCTGGGTGGGGGGTTGCTGTGCTGCACTT
GCCCCCTCGGGGGGGTCCCAGGGCCCCAGCCATTACATGGCCCCGCTACTCAACATCTGCCCCCT
GCCATCTCTCGGGGGGCCCTCTGAGTACCCTACCAAGAATTACGTCTTGACGTGGAGGGGAATG
GGGGCTCCGCTGGCGCTAGAGCCATCCAGAAGTGGCAGTGCCCAACAGCTTTGGGATGGGTT
CGTACCTTTTGTCTCTGCCTCCTGCTATTTTTCTTTTGACTGAGGATATTTAAAATTCATTT
GAAAACCTGAGCCAAGGTGTTGACTCAGACTCTCACTTAGGCTCTGCTGTTTCTCACCCCTTGG
ATGATGGAGCCAAAGAGGGGATGCTTTGAGATTCTGGATCTTGACATGCCCATCTTAGAAGC
CAGTCAAGCTATGGAACATAATGCGGAGGCTGCTTGCTGTGCTGGCTTTGCAACAAGACAGAC
TGTCCTCCAAGAGTTCCTGCTGCTGCTGGGGGCTGGGCTTCCCTAGATGTCACTGGACAGCTG
CCCCCATCCTACTCAGGTCTCTGGAGCTCCTCTCTTACCCCTGGAAAAACAAATCATCTG
TTAACAAAGGACTGCCACCTCCGGAACCTCTGACCTCTGTTTCCCTCCGTCCTGATAAGACG
TCCACCCCCCAGGGCCAGGTCCCAGCTATGTAGACCCCCGCCCCACCTCCAACACTGCACC
CTTCTGCCCTGCCCCCCTCGTCTCACCCCCTTTTACACTCACATTTTTATCAAATAAAGCATG
TTTTGTTAGTGCA

FIGURE 190

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73736

><subunit 1 of 1, 220 aa, 1 stop

><MW: 23292, pI: 8.43, NX(S/T): 0

MASAGMQILGVVLTLLGWVNGLVSCALPMWKVTAFIGNSIVVAQVVWEGWLMSCVVQSTGQM
QCKVYDSLALPQDLQAARALCVIALLVALLFGLLVYLAGAKCTTCVEEKDSKARLVLTSGIV
FVISGVLTLIPVCWTAHAIIRDFYNPLVAEAQKRELGASLYLGWAASGLLLLGGGLLCCTCP
SGGSQGPPSHYMARYSTSAPAIISRGPPSEYPTKNYV

Transmembrane domains:

amino acids 8-30 (type II), 82-102, 121-140, 166-186

193/270

FIGURE 191

GCCAAGGAGAACATCATCAAAGACTTCTCTAGACTCAAAGGCTTCCACGTTCTACATCTTG
AGCATCTTCTACCACTCCGAATTGAACCACTCTTCAAAGTAAAGGCAATGGCATTTTATCCC
TTGCAAATTGCTGGGCTGGTTCTTGGGTTCTTGGCATGGTGGGGACTCTTGCCACAACCCCT
TCTGCCTCAGTGGTGGAGTATCAGCTTTTGTGGCAGCAACATTATTGTCTTTGAGAGGCTC
TGGGAAGGGCTCTGGATGAATTGCATCCGACAAGCCAGGGTCCGGTTGCAATGCAAGTTCTA
TAGCTCCTTGTTGGCTCTCCCGCCTGCCCTGGAAACAGCCCGGGCCCTCATGTGTGTGGCTG
TTGCTCTCTCCTTGATCGCCCTGCTTATTGGCATCTGTGGCATGAAGCAGGTCCAGTGCACA
GGCTCTAACGAGAGGGCCAAAGCATACTTCTGGGAACTTCAGGAGTCTCTTTCATCCTGAC
GGGTATCTTCGTTCTGATTCCGGTGAGCTGGACAGCCAATATAATCATCAGAGATTTCTACA
ACCCAGCCATCCACATAGGTCAGAAACGAGAGCTGGGAGCAGCACTTTTCCTTGGCTGGGCA
AGCGCTGCTGTCCTCTTCATTGGAGGGGGTCTGCTTTGTGGATTTTGCTGCTGCAACAGAAA
GAAGCAAGGGTACAGATATCCAGTGCCTGGCTACCGTGTGCCACACACAGATAAGCGAAGAA
ATACGACAATGCTTAGTAAGACCTCCACCAGTTATGTCTTAATGCCTCCTTTTGGCTCCAAGT
ATGGACTATGGTCAATGTTTTTTATAAAGTCCTGCTAGAACTGTAAGTATGTGAGGCAGGA
GAACTTGCTTTATGTCTAGATTTACATTGATACGAAAGTTTCAATTTGTTACTGGTGGTAGG
AATGAAAATGACTTACTTGGACATTCTGACTTCAGGTGTATTAAATGCATTGACTATTGTTG
GACCCAATCGCTGCTCCAATTTTCATATTCTAAATTCAAGTATACCATAATCATTAGCAAG
TGTACAATGATGGACTACTTATTACTTTTTGACCATCATGTATTATCTGATAAGAATCTAAA
GTTGAAATTGATATTCTATAACAATAAAACATATACCTATTCTA

194/270

FIGURE 192

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73737

><subunit 1 of 1, 173 aa, 1 stop

><MW: 18938, pI: 9.99, NX(S/T): 1

MNCIRQARVRLQCKFYSSLLALPPALETARALMCVAVALSLIALLLIGICGMKQVQCTGSNER
AKAYLLGTSGVLFILTGIFVLIPVSWTANIIIRDFYNPAIHIGQKRELGAALFLGWASAAVL
FIGGGLLCGFCCCNRRKKQGYRYPVPGYRVPHTDKRRNTTMLSSTSYV

Important features of the protein:

Transmembrane domains:

amino acids 31-51, 71-90, 112-133

N-glycosylation site.

amino acids 161-164

FIGURE 193

AGTGACAATCTCAGAGCAGCTTCTACACCACAGCCATTTCCAGCATGAAAGATCACTGGGGGT
CTCCTTCTGCTCTGTACAGTGGTCTATTTCTGTAGCAGCTCAGAAGCTGCTAGTCTGTCTCC
AAAAAAAGTGGACTGCAGCATTTACAAGAAGTATCCAGTGGTGGCCATCCCCTGCCCCATCA
CATACTACCAGTTTGTGGTTCTGACTACATCACCTATGGGAATGAATGTCACTTGTGTACC
GAGAGCTTGAAAAGTAATGGAAGAGTTCAGTTTCTTCACGATGGAAGTTGCTTAAATTCTCCA
TGGACATAGAGAGAAAGGAATGATATTCTCATCATCATCTTCATCATCCCAGGCTCTGACTG
AGTTTCTTTTCAGTTTACTGATGTTCTGGGTGGGGGACAGAGCCAGATTCAGAGTAATCTTG
ACTGAATGGAGAAAGTTTCTGTGCTACCCCTACAAACCCATGCCTCACTGACAGACCAGCAT
TTTTTTTTTAACACGTCAATAAAAAAATAATCTCCCAGA

FIGURE 194

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73739

><subunit 1 of 1, 85 aa, 1 stop

><MW: 9232, pI: 7.94, NX(S/T): 0

MKITGGLLLLCTVVYFCSSSEAASLSPKKVDCSIYKKYPVVAIPCPITYLPVCGSDYITYGN

ECHLCTESLKSNQGRVQFLHDGSC

Signal peptide:

amino acids 1-19

FIGURE 195

CCCGCGCCCGGTTCTCCCTCGCAGCACCTCGAAGTGCGCCCTCGCCCTCCTGCTCGCGCCC
CGCCGCCATGGCTGCCTCCCCGCGCGGCCTGCTGTCCTGGCCCTGACCGGGCTGGCGCTGC
TCCTGCTCCTGTGCTGGGGCCCAGGTGGCATAAGTGGAATAAACTCAAGCTGATGCTTCAA
AAACGAGAAGCACCTGTTCCAATAAGACTAAAGTGGCCGTTGATGAGAATAAAGCCAAAGA
ATTCCTTGGCAGCCTGAAGCGCCAGAAGCGGCAGCTGTGGGACCGGACTCGGCCCCGAGGTGC
AGCAGTGGTACCAGCAGTTTCTCTACATGGGCTTTGATGAAGCGAAATTTGAAGATGACATC
ACCTATTGGCTTAACAGAGATCGAAATGGACATGAATACTATGGCGATTACTACCAACGTCA
CTATGATGAAGACTCTGCAATTGGTCCCCGGAGCCCCCTACGGCTTTAGGCATGGAGCCAGCG
TCAACTACGATGACTACTTAACCATGACTTGCCACACGCTGTACAAGAAGCAAATAGCGATTCT
TCTTCATGTATCTCCTAATGCCTTACACTACTTGGTTTCTGATTTGCTCTATTTTCAGCAGAT
CTTTTCTACCTACTTTGTGTGATCAAAAAAGAAGAGTTAAACAACACATGTAAATGCCTTT
TGATATTTTCATGGGAATGCCTCTCATTTAAAAATAGAAATAAAGCATTTTGTAAAAAGA

FIGURE 196

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73742

><subunit 1 of 1, 148 aa, 1 stop

><MW: 17183, pI: 8.77, NX(S/T): 0

MAASPARPAVLALTGLALLLLLCWGPGGISGNKCLKMLQKREAPVPTKTKVAVDENKAKEFL
GSLKRQKRQLWDRTRPEVQQWYQQFLYMGFDEAKFEDDITYWLNDRNGHEYYGDDYYQRHYD
EDSAIGPRSPYGFRHGASVNYDDY

Signal peptide:

amino acids 1-30

199/270

FIGURE 197

CGGCTCGAGCCCGCCCGGAAGTGCCCGAGGGGCGCGATGGAGCTGGGGGAGCCGGGCGCTC
GGTAGCGCGGCGGGCAAGGCAGGCGCCATGACCCTGATTGAAGGGGTGGGTGATGAGGTGAC
CGTCCTTTTCTCGGTGCTTGCCTGCCTTCTGGTGCTGGCCCTTGCCTGGGTCTCAACGCACA
CCGCTGAGGGCGGGGACCCACTGCCCCAGCCGTCAGGGACCCCAACGCCATCCCAGCCCAGC
GCAGCCATGGCAGCTACCGACAGCATGAGAGGGGAGGCCCCAGGGGCAGAGACCCCCAGCCT
GAGACACAGAGGTCAAGCTGCACAGCCAGAGCCCAGCACGGGGTTCACAGCAACACCGCCAG
CCCCGGA CTCCCCGAGGAGCCCCTCGTGCTACGGCTGAAATTCTCTCAATGATTTCAGAGCAG
GTGGCCAGGGCCTGGCCCCACGACACCATTGGCTCCTTGAAAAGGACCCAGTTTCCCGGCCG
GGAACAGCAGGTGCGACTCATCTACCAAGGGCAGCTGCTAGGCGACGACACCCAGACCCTGG
GCAGCCTTCACCTCCCTCCCAACTGCGTTCTCCACTGCCACGTGTCCACGAGAGTCGGTCCC
CCAAATCCCCCTGCCCCGCCGGGGTCCGAGCCCGGCCCTCCGGGCTGGAAATCGGCAGCCT
GCTGCTGCCCCCTGCTGCTCCTGCTGTTGCTGCTGCTCTGGTACTGCCAGATCCAGTACCGGC
CCTTCTTTCCCTGACCGCCACTCTGGGCCTGGCCGGCTTCACCCTGCTCCTCAGTCTCCTG
GCCTTTGCCATGTACCGCCCCGTAGTGCCTCCGCGGGCGCTTGGCAGCGTCGCCGGCCCCCTCC
GGACCTTGCTCCCCGCGCCGCGGCGGGAGCTGCTGCCTGCCAGGCCCGCCTCTCCGGCCTG
CCTCTTCCCGCTGCCCTGGAGCCCAGCCCTGCGCCGAGAGGACTCCCGGGACTGGCGGAGG
CCCCGCCCTGCGACCGCCGGGGCTCGGGGCCACCTCCCGGGGCTGCTGAACCTCAGCCCGCA
CTGGGAGTGGGCTCCTCGGGGTGCGGCATCTGCTGTGCTGCCTCGGCCCCGGGCAGAGCCG
GGCCGCCCCGGGGGCCCGTCTTAGTGTTCTGCCGAGGACCCAGCCGCCTCCAATCCCTGAC
AGCTCCTTGGGCTGAGTTGGGGACGCCAGGTCCGTGGGAGGCTGGTGAAGGGGAGCGGGGAG
GGGCAGAGGAGTTCCCCGGAACCCGTGCAGATTAAAGTAACTGTGAAGTTTTAAAAAAAAAA
AAAAAAA

200/270

FIGURE 198

MTLIEGVGDEVTVLFSVLACLLVLALAWVSTHTAEGGDPLPQPSGTPTPSQPSAAMAATDSM
RGEAPGAETPSLRHRGQAAQPEPSTGFTATPPAPDSPQEPLVLRLLKFLNDSEQVARAWPHDT
IGSLKRTQFPGREQQVRLIYQGQLLGDDTQTLGSLHLPPNCVLHCHVSTRVGPPNPPCPPGS
EPGPSGLEIGSLLLPLLLLLLLLLLWYCQIQYRPFPLTATLGLAGFTLLLSLLAFAMYRP

Signal peptide:

amino acids 1-31

Transmembrane domain:

amino acids 195-217

201/270

FIGURE 200

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73746

><subunit 1 of 1, 148 aa, 1 stop

><MW: 16896, pI: 6.05, NX(S/T): 1

MTKALLIYLVSSFLALNQASLISRCDLAQVLQLEDLDGFEGLSDWLCLAFVESKFNISKI

NENADGSFDYGLFQINSHYWCNDYKSYSENLC HVDCQDLLNP NLLAGIHCAKRIVSGARGMN

NWVEWRLHCSGRPLSYWLTGCRLR

Signal peptide:

amino acids 1-18

FIGURE 201

TCTGACCTGACTGGAAGCGTCCAAAGAGGGACGGCTGTGAGCCCTGCTTGACTGAGAACCCA
CCAGCTCATCCCAGACACCTCATAGCAACCTATTTATACAAAGGGGGAAAGAAACACCTGAG
CAGAATGGAATCATTATTTTTTTTCCCAAGGAGAAAACCGGGGTAAAGGGAGGGAAGCAATTC
AATTTGAAGTCCCTGTGAATGGGCTTTCAGAAGGCAATTAAAGAAATCCACTCAGAGAGGAC
TTGGGGTGAACTTGGGTCTGTGGTTTTCTGATTGTAAGTGGAAGCAGGTCTTGACACACGC
TGTTGGCAAATGTCAGGACCAGGTTAAGTGACTGGCAGAAAACTTCCAGGTGGAACAAGCA
ACCCATGTTCTGCTGCAAGCTTGAAGGAGCCTGGAGCGGGAGAAAGCTAACTTGAACATGAC
CTGTTGCATTTGGCAAGTTCTAGCAACATGCTCCTAAGGAAGCGATACAGGCACAGACCATG
CAGACTCCAGTTCCTCCTGCTGCTCCTGATGCTGGGATGCGTCCTGATGATGGTGGCGATGT
TGCACCCCTCCCCACCACACCCTGCACCAGACTGTCACAGCCCAAGCCAGCAAGCACAGCCCT
GAAGCCAGGTACCGCCTGGACTTTGGGGAATCCCAGGATTGGGTACTGGAAGCTGAGGATGA
GGGTGAAGAGTACAGCCCTCTGGAGGGCCTGCCACCCTTTATCTCACTGCGGGAGGATCAGC
TGCTGGTGGCCGTGGCCTTACCCCAGGCCAGAAGGAACCAGAGCCAGGGCAGGAGAGGTGGG
AGCTACCGCCTCATCAAGCAGCCAAGGAGGCAGGATAAGGAAGCCCCAAAGAGGGGACTGGGG
GGCTGATGAGGACGGGGAGGTGTCTGAAGAAGAGGAGTTGACCCCGTTCAGCCTGGACCCAC
GTGGCCTCCAGGAGGCACTCAGTGCCCGCATCCCCCTCCAGAGGGCTCTGCCCGAGGTGCGG
CACCCACTGTGTCTGCAGCAGCACCCCTCAGGACAGCCTGCCACAGCCAGCGTCATCCTCTG
TTTCCATGATGAGGCCTGGTCCACTCTCCTGCGGACTGTACACAGCATCCTCGACACAGTGC
CCAGGGCCTTCCCTGAAGGAGATCATCCTCGTGGACGACCTCAGCCAGCAAGGACAACTCAAG
TCTGCTCTCAGCGAATATGTGGCCAGGCTGGAGGGGGTGAAGTTACTCAGGAGCAACAAGAG
GCTGGGTGCCATCAGGGCCCGGATGCTGGGGGCCACCAGAGCCACCGGGGATGTGCTCGTCT
TCATGGATGCCCCTGCGAGTGCCACCCAGGCTGGCTGGAGCCCCTCCTCAGCAGAATAGCT
GGTGACAGGAGCCGAGTGATCTCCGGTGATAGATGTGATTGACTGGAAGACTTTCAGTA
TTACCCCTCAAAGGACCTGCAGCGTGGGGTGTGGACTGGAAGCTGGATTTCCACTGGGAAC
CTTTGCCAGAGCATGTGAGGAAGGCCCTCCAGTCCCCCATAAGCCCCATCAGGAGCCCTGTG
GTGCCCCGAGAGGTGGTGGCCATGGACAGACATTACTTCCAAAACACTGGAGCGTATGACTC
TCTTATGTGCTGCGAGGTGGTGA AACCTCGAACTGTCTTTCAAGGCCTGGCTCTGTGGTG
GCTCTGTTGAAATCCTTCCCTGCTCTCGGGTAGGACACATCTACCAAATCAGGATTCCCAT
TCCCCCTCGACCAGGAGGCCACCCTGAGGAACAGGGTTCGCATTGCTGAGACCTGGCTGGG
GTCATTCAAAGAAACCTTCTACAAGCATAGCCCAGAGGCCTTCTCCTTGAGCAAGGCTGAGA
AGCCAGACTGCATGGAACGCTTGCAAGCTGCAAAGGAGACTGGGTTGTGCGACATTCCACTGG
TTTCTGGCTAATGTCTACCCTGAGCTGTACCCATCTGAACCCAGGCCAGTTTCTCTGAAA
GCTCCACAACACTGGACTTGGGCTCTGTGCAGACTGCCAGGCAGAAGGGGACATCCTGGGCT
GTCCCATGGTGTGGCTCCTTGCAAGTACAGCCGGCAGCAACAGTACCTGCAGCACACCAGC
AGGAAGGAGATTCACTTTGGCAGCCCACAGCACCTGTGCTTTGCTGTGAGGAGGAGGAGG
GATTCTTCAGAACTGCACGGAGGAAGGCCTGGCCATCCACCAGCAGCACTGGGACTTCCAGG
AGAATGGGATGATTGTCCACATTCTTTCTGGGAAATGCATGGAAGCTGTGGTGCAAGAAAAC
AATAAGATTGTGACCTGCGTCCGTGTGATGGAAAAGCCCGCCAGCAGTGGCGATTGTGACCA
GATAAATGCTGTGGATGAACGATGAATGTCAATGTGAGAAGGAAAAGAGAATTTTGGCCATC
AAAATCCAGCTCCAAGTGAACGTAAAGAGCTTATATATTTTCATGAAGCTGATCCTTTTGTGT
GTGTGCTCCTTGTGTTAGGAGAGAAAAAGCTCTATGAAAGAATATAGGAAGTTTCTCCTTT
TCACACCTTATTTTCATTGACTGCTGGCTGCTTA

FIGURE 202

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73760

><subunit 1 of 1, 639 aa, 1 stop

><MW: 73063, pI: 6.84, NX(S/T): 2

MLLRKRYRHRPCRLQFLLLLLMLGCVLMMVAMLHPPHHTLHQT VTAQASKHSPEARYRLDFG
ESQDWVLEAEDEGE EYSPL EGLPPFISLREDQLLVAVALPQARRNQSQGRRGGSYRLIKQPR
RQDKEAPKRDWGADEDEGEVSEEEELTPFSLDPRGLQEALSARIPLQRALPEVRHPLCLQQHP
QDSLPTASVILCFHDEAWSTLLRTVHSILDTVPRAFLKEIILVDDLSQQGQLKSALSEYVAR
LEGVKLLRSNKRLGAIRARMLGATRATGDVLVFMDAHCECHPGWLEPLLSRIAGDRSRVVSP
VIDVIDWKTFQYYPSKDLQRGVLDWKLDHFHWEPLPEHVRKALQSPISPIRSPVVPGEVVAMD
RHYFQNTGAYDSLMSLRGGENLELSFKAWLCGGSVEILPCSRVGHIYQNQDSHSPLDQEATL
RNRVRIAETWLGSFKETFYKHSPEAFSLSKAEKPDCEMERLQLQRRLLGCRTFHWFLANVYPEL
YPSEPRPSFSGKLHNTGLGLCADCQAEGDILGCPMVLAPCSDSRQQQYLQHTSRKEIHFGSP
QHLCFAVRQEQVILQNCTEEGLAIHQHWD FQENGMIVHILSGKCMEAVVQENNKDLYLRPC
DGKARQQWRFDQINAVDER

Signal peptide:

amino acids 1-28

265/270

FIGURE 203

CGCCAAGCATGCAGTAAAGGCTGAAAATCTGGGTACAGCTGAGGAAGACCTCAGACATGGA
GTCCAGGATGTGGCCTGCGCTGCTGCTGTCCCACCTCCTCCCTCTCTGGCCACTGCTGTTGC
TGCCCCCTCCCACCGCCTGCTCAGGGCTCTTCATCCTCCCCCTCGAACCCACCAGCCCCAGCC
CGCCCCCGTGTGCCAGGGGAGGCCCCCTCGGCCCCACGTATGTGTGCGTGTGGGAGCGAGC
ACCTCCACCAAGCCGATCTCCTCGGGTCCCAAGATCACGTCGGCAAGTCCTGCCTGGCACTG
CACCCCCAGCCACCCCATCAGGCTTTGAGGAGGGGCGCCCTCATCCCAATACCCCTGGGCT
ATCGTGTGGGGTCCCACCGTGTCTCGAGAGGATGGAGGGGACCCCAACTCTGCCAATCCCGG
ATTTCTGGACTATGGTTTTGACAGCCCTCATGGGCTCGCAACCCACACCCCAACTCAGACT
CCATGCGAGGTGATGGAGATGGGCTTATCCTTGAGAGGACCTGCCACCCTGCGGCCATTC
CTGTTCTGGGGGCGGTGGGGAAGGTGTGGACCCCCAGCTCTATGTCACAATTACCATCTCCAT
CATCATTGTTCTCGTGGCCACTGGCATCATCTTCAAGTTCTGCTGGGACCGCAGCCAGAAGC
GACGCAGACCCTCAGGGCAGCAAGGTGCCCTGAGGCAGGAGGAGAGCCAGCAGCCACTGACA
GACCTGTCCCCGGCTGGAGTCACTGTGCTGGGGGCTTCGGGGACTCACCTACCCCCACCCC
TGACCATGAGGAGCCCCGAGGGGACCCCGGCTGGGATGCCCCACCCCAAGGGGGCTCCAG
CCTTCCAGTTGAACCGGTGAGAGGGCAGGGGCAATGGGATGGGAGGGCAAAGAGGGGAAGGCAAC
TTAGGTCTTCAGAGCTGGGGTGGGGGTGCCCTCTGGATGGGTAGTGAGGAGGCAGGCGTGGC
CTCCCACAGCCCCCTGGCCCTCCCAAGGGGGCTGGACCAGCTCCTCTCTGGGAGGCACCCTTC
CTTCTCCAGTCTCTCAGGATCTGTGTCTATTCTCTGCTGCCATAACTCCAACCTCTGCCC
TCTTTGGTTTTTTCTCATGCCACCTTGTCTAAGACAACCTCTGCCCTCTTAACCTTGATTCCC
CCTCTTTGTCTTGAACCTTCCCCTTCTATTCTGGCCTACCCCTTGTTTCTGACTGTGCCCTT
TCCCTCTTCCTCTCAGGATTCCTTGGTGAATCTGTGATGCCCCAATGTTGGGGTGCAGCC
AAGCAGGAGGCCAAGGGGCCGGCACAGCCCCCATCCCCTGAGGGTGGGGCAGCTGTGGGGA
GCTGGGGCCACAGGGGCTCCTGGCTCCTGCCCCTTGACACACCACCCGGAACACTCCCCAGCC
CCACGGGCAATCCTATCTGCTCGCCCTCCTGCAGGTGGGGGCTCACATATCTGTGACTTCG
GGTCCCTGTCCCCACCCTTGTGCACTCACATGAAAGCCTTGACACTCACCTCCACCTTCAC
AGGCCATTTGCACACGCTCCTGCACCCTCTCCCCGTCCATAACCGCTCCGCTCAGCTGACTCT
CATGTTCTCTCGTCTCACATTTGCACTCTCTCCTTCCCACATTCTGTGCTCAGCTCACTCAG
TGGTCAGCGTTTCTGACACTTTACCTCTCATGTGCGTTTCCCGGCTGATGTTGTGGTGG
TGTGCGGCGTGCTCACTCTCTCCCTCATGAACACCCACCCACCTCGTTTCCGCAGCCCCCTGC
GTGCTGCTCCAGAGGTGGGTGGGAGGTGAGCTGGGGGCTCCTTGGGCCCTCATCGGTCATGG
TCTCGTCCCATTCCACACCATTGTTTCTGTCTCCCCATCCTACTCCAAGGATGCCGGCA
TCACCCTGAGGGCTCCCCCTTGGGAATGGGGTAGTGAGGCCCCAGACTTCACCCCCAGCCCA
CTGCTAAAATCTGTTTTCTGACAGATGGGTTTTGGGGAGTCGCCTGCTGCACTACATGAGAA
AGGGACTCCCATTGCCCCTTCCCTTTCTCCTACAGTCCCTTTTGTCTTGTCTGCTCCTGGCTG
TCTGTGTGTGTGCCATTCTCTGGACTTCAGAGCCCCCTGAGCCAGTCCTCCCTTCCCAGCCT
CCCTTTGGGCCTCCCTAACTCCACCTAGGCTGCCAGGGACCGGAGTCAGCTGGTTCAAGGCC
ATCGGGAGCTCTGCCTCCAAGTCTACCCTTCCCTTCCCGGACTCCCTCCTGTCCCCTCCTTT
CCTCCCTCCTTCCCTTCCACTCTCCTTCCCTTTTGCTTCCCTGCCCTTTCCCCCTCCTCAGGTT
CTTCCCTCCTTCTCACTGGTTTTTCCACCTTCTCCTTCCCTTCTTCCCTGGCTCCTAGGCT
GTGATATATATTTTTGTATTATCTCTTTCTTCTTGTGGTGATCATCTTGAATTACTGTG
GGATGTAAGTTTTCAAATTTTCAAATAAAGCCTTTGCAAGATAA

FIGURE 204

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76393

><subunit 1 of 1, 243 aa, 1 stop

><MW: 26266, pI: 8.43, NX(S/T): 1

MRPQGPAASPQRLRGLLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPAGV
PGRDGSPGANVIPGTPGIPGRDGFKEKGECLRESFEESWTPNYKQCSWSSLNYGIDLGKIA
ECTFTKMRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECGGLPIEAI IYLDQGSPEMN
STINIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSR I I I EELPK

Signal peptide:

amino acids 1-30

Transmembrane domain:

amino acids 195-217

FIGURE 205

GTTAACCAGCGCAGTCCTCCGTGCGTCCCGCCCGCCGCTGCCCTCACTCCCGGCCAGGATGG
CATCCTGTCTGGCCCTGCGCATGGCGCTGCTGCTGGTCTCCGGGGTTCTGGCCCCCTGCGGTG
CTCACAGACGATGTTCCACAGGAGCCCGTGCCACGCTGTGGAACGAGCCGGCCGAGCTGCC
GTCGGGAGAAGGCCCCGTGGAGAGCACCAGCCCCGGCCGGGAGCCCGTGGACACCGGTCCCC
CAGCCCCCACCCTCGCGCCAGGACCCGAGGACAGCACC GCGCAGGAGCGGCTGGACCAGGGC
GGCGGGTCGCTGGGGCCCCGGCGCTATCGCGGCCATCGTGATCGCCGCCCTGCTGGCCACCTG
CGTGGTGCTGGCGCTCGTGGTCTGTCGCGCTGAGAAAGTTTTCTGCCTCCTGAAGCGAATAAA
GGGGCCGCGCCCGGCCGCGGCGCGACTCGGCAAAAAAAAAAAAAAAAAA

FIGURE 206

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76398

><subunit 1 of 1, 121 aa, 1 stop

><MW: 12073, pI: 4.11, NX(S/T): 0

MASCLALRMALLLVSGVLAPAVLTDDVPQEPVPTLWNEPAELPSGEGPVESTSPGREPVDTG
PPAPTVPAGPEDSTAQERLDQGGSLGPGAIAAIVIAALLATCVVLALVVVALRKFSAS

Important features of the protein:

Signal peptide:

amino acids 1-19

Transmembrane domain:

amino acids 91-110

Glycosaminoglycan attachment site.

amino acids 44-47

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 116-119

N-myristoylation site.

amino acids 91-96

FIGURE 207

GGCCGTTGGTTGGTGCGCGGCTGAAGGGTGTGGCGCGAGCAGCGTCGTTGGTTGGCCGGCGG
CGGGCCGGGACGGGCATGGCCCTGCTGCTGTGCCTGGTGTGCCTGACGGCGGCGCTGGCCCA
CGGCTGTCTGCACTGCCACAGCAACTTCTCCAAGAAGTTCTCCTTCTACCGCCACCATGTGA
ACTTCAAGTCCTGGTGGGTGGGCGACATCCCCGTGTCAGGGGCGCTGCTCACCAGCTGGAGC
GACGACACGATGAAGGAGCTGCACCTGGCCATCCCCGCCAAGATCACCCGGGAGAAGCTGGA
CCAAGTGGCGACAGCAGTGTACCAGATGATGGATCAGCTGTACCAGGGGAAGATGTACTTCC
CCGGGTATTTCCCCAACGAGCTGCGAAACATCTTCCGGGAGCAGGTGCACCTCATCCAGAAC
GCCATCATCGAAAGGCACCTGGCACCAGGCAGCTGGGGAGGAGGGCAGCTCTCCAGGGAGGG
ACCCAGCCTAGCACCTGAAGGATCAATGCCATCACCCCGCGGGGACCTCCCCTAAGTAGCCC
CCAGAGGCGCTGGGAGTGTGTCACCGCCCTCCCCCTGAAGTTTGCTCCATCTCACGCTGGGG
GTCAACCTGGGGACCCCTTCCCTCCGGGCCATGGACACACATACATGAAAACCAGGCCGCAT
CGACTGTCAGCACCGCTGTGGCATCTTCCAGTACGAGACCATCTCCTGCAACAACTGCACAG
ACTCGCACGTGCGCTGCTTTGGCTATAACTGCGAGTAGGGCTCAGGCATCACACCCACCCGT
GCCAGGGCCCTACTGTCCCTGGGGTCCCAGGCTCTCCTTGGAGGGGGCTCCCCGCCTTCCAC
CTGGCTGTCAATCGGGTAGGGCGGGGCCGTGGGTTTCAGGGGCGCACCCTTCCAAGCCTGTGT
CCCACAGGTCCTCGGCGCAGTGGAAGTCAGCTGTCCAGGGCCTCCTGAACTACATAAATAAC
TGGCACAAGTAAGTCCCCTCCTCAAACCAACACAGGCAGTGTGTGTATGTGAGCACCTCGTG
GGTGAGTATGTGTGGGGCACAGGCTGGCTCCCTCAGCTCCACGTCCTAGAGGGGGCTCCCGA
GGAGGTGGAACCTCAACCCAGCTCTGCGCAGGAGGCGGCTGCAGTCCTTTTCTCCCTCAAAG
GTCTCCGACCCTCAGCTGGAGGCGGGCATCTTTCCTAAAGGGTCCCCATAGGGTCTGGTTCC
ACCCCATCCCAGGTCTGTGGTCAGAGCCTGGGAGGGTTCCTACGATGGTTAGGGGTGCCCC
ATGGAGGGGCTGACTGCCCCACATTGCCTTTTCAGACAGGACACGAGCATGAGGTAAGGCCGC
CCTGACCTGGACTTCAGGGGGAGGGGGTAAAGGGAGAGAGGAGGGGGGCTAGGGGGTCTCT
AGATCAGTGGGGGCACTGCAGGTGGGGCTCTCCCTATACCTGGGACACCTGCTGGATGTCAC
CTCTGCAACCACACCCATGTGGTGGTTTCATGAACAGACCACGCTCCTCTGCCTTCTCCTGG
CCTGGGACACACAGAGCCACCCCGGCCTTGTGAGTGACCCAGAGAAGGGAGGCCTCGGGAGA
AGGGGTGCTCGTAAGCCAACACCAGCGTGCCGCGGCCTGCACACCCTTCGGACATCCCAGGC
ACGAGGGTGTGCTGGATGTGGCCACACATAGGACCACACGTCCTCAGCTGGGAGGAGAGGCCT
GGGGCCCCCAGGGAGGGAGGCAGGGGGTGGGGGACATGGAGAGCTGAGGCAGCCTCGTCTCC
CCGACGCTGGTATCGCCAGCCTTAAGGTGTCTGGAGCCCCACACTGGCCAACCTGACCT
TGGAAGATGCTGCTGAGTGTCTCAAGCAGCACTGACAGCAGCTGGGCCTGCCCCAGGGCAAC
GTGGGGGCGGAGACTCAGCTGGACAGCCCCTGCCTGTCACTCTGGAGCTGGGCTGCTGCTGC
CTCAGGACCCCTCTCCGACCCCGACAGAGCTGAGCTGGCCAGGGCCAGGAGGGCGGGAGG
GAGGGAATGGGGGTGGGCTGTGCGCAGCATCAGCGCCTGGGCAGGTCCGCAGAGCTGCGGGA
TGTGATTAAAGTCCCTGATGTTTCTC

FIGURE 208

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76399

><subunit 1 of 1, 157 aa, 1 stop

><MW: 17681, pI: 7.65, NX(S/T): 1

MALLLCLVCLTAALAHGCLHCHSNFSKKFSFYRHVNFKSWWVGDI PVSGALLTDWSDDTMK

ELHLAIPAKITREKLDQVATAVYQMDQLYQGKMYFPGYFPNELRNIFREQVHLIQNAIIER

HLAPGSWGGGQLSREGPSLAPEGSMPSPRGDLP

Signal peptide:

amino acids 1-15

FIGURE 209

AGCAGGAGCAGGAGAGGGACAATGGGAAGCTGCCCCGTCCAGGTTTCATGTTCTCTTATTTCT
CCTCACGTGTGAGCTGGCTGCAGAAGTTGCTGCAGAAGTTGAGAAATCCTCAGATGGTCCTG
GTGCTGCCCAGGAACCCACGTGGCTCACAGATGTCCCAGCTGCCATGGAATTCATTGCTGCC
ACTGAGGTGGCTGTCATAGGCTTCTTCCAGGATTTAGAAATACCAGCAGTGCCCATACTCCA
TAGCATGGTGCAAAAATTCCCAGGCGTGTCATTTGGGATCAGCACTGATTCTGAGGTTCTGA
CACACTACAACATCACTGGGAACACCATCTGCCTCTTTTCGCCTGGTAGACAATGAACAACTG
AATTTAGAGGACGAAGACATTGAAAGCATTGATGCCACCAAATTGAGCCGTTTTATTGAGAT
CAACAGCCTCCACATGGTGACAGAGTACAACCCTGTGACTGTGATTGGGTTATTCAACAGCG
TAATTCAGATTCATCTCCTCCTGATAATGAACAAGGCCTCCCCAGAGTATGAAGAGAACATG
CACAGATACCAGAAGGCAGCCAAGCTCTTCCAGGGGAAGATTCTCTTTATTCTGGTGGACAG
TGGTATGAAAGAAAATGGGAAGGTGATATCATTTTTTCAAATAAGGAGTCTCAACTGCCAG
CTTTGGCAATTTACCAGACTCTAGATGACGAGTGGGATACACTGCCCACAGCAGAAGTTTCC
GTAGAGCATGTGCAAACTTTTGTGATGGATTCTTAAGTGGAATAATTGTTGAAAGAAAATCG
TGAATCAGAAGGAAAGACTCCAAAGGTGGAACCTCTGACTTCTCCTTGGAACACATATGGCC
AAGTATCTACTTTATGCAAAGTAAAAAGGCACAACCTCAAATCTCAGAGACACTAAACAACAG
GATCACTAGGCCTGCCAACACACACACACGACGACGTGCACACACGCACGCACGCGTGACAC
ACACACGCGCACACACACACACACAGAGCTTCATTTCTGTCTTAAATCTCGTTTTCTC
TTCTTCCTTCTTTTAAATTTTCATATCCTCACTCCCTATCCAATTTCTTCTTATCGTGATT
CATACTCTGTAAGCCCATCTGTAACACACCTAGATCAAGGCTTTAAGAGACTCACTGTGATG
CCTCTATGAAAGAGAGGCATTCCTAGAGAAAGATTGTTCCAATTTGTCATTTAATATCAAGT
TTGTATACTGCACATGACTTACACACAACATAGTTCCTGCTCTTTTAAGGTTACCTAAGGGT
TGAAACTCTACCTTCTTTCATAAGCACATGTCCGTCTCTGACTCAGGATCAAAAACCAAAGG
ATGGTTTTAAACACCTTTGTGAAATTGTCTTTTTGCCAGAAGTTAAAGGCTGTCTCCAAGTC
CCTGAACTCAGCAGAAATAGACCATGTGAAACTCCATGCTTGGTAGCATCTCCAACCTCCC
TATGTAAATCAACAACCTGCATAATAATAAAAGGCAATCATGTTATA

FIGURE 210

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76401

><subunit 1 of 1, 273 aa, 1 stop

><MW: 30480, pI: 4.60, NX(S/T): 1

MEAAPSRFMFLFLLTCELAAEVAAEVEKSSDGPAAQEPTWLTDVPAAMEFIAATEVAVIG
FFQDLEIPAVPILHSMVQKFPGVSGISTDSEVLTHYNITGNTICLFRRLVDNEQLNLEDEDI
ESIDATKLSRFIEINSLHMTVEYNPVTVIGLFNSVIQIHLLIMNKASPEYEENMHRYQKAA
KLFQGKILFILVDSGMKENGKVISFFKLKESQLPALAIYQTLDDDEWDTLPTAEVSVEHVQNF
CDGFLSGKLLKENRESEGKTPKVEL

Signal peptide:

amino acids 1-20

Transmembrane domain:

amino acids 143-162

213/270

FIGURE 211

GGAGAGCCGCGGCTGGGACCGGAGTGGGGAGCGCGGCGTGAGGTGCCACCCGGCGCGGGTG
GCGGAGAGATCAGAAGCCTCTTCCCCAAGCCGAGCCAACCTCAGCGGGGACCCGGGCTCAGG
GACGCGGCGGCGGCGGCGGCGGCGACTGCAGTGGCTGGACGATGGCGAGCGTCCGCCGGAGCCGGG
GCGGTGATTGCAGCCCCAGACAGCCGGCGCTGGCTGTGGTGGTGGTGGCGGCGGCGCTTG
GCTCTTGACAGCTGGAGTATCAGCCTTGGAAGTATATACGCCAAAAGAAATCTTCGTGGCAA
ATGGTACACAAGGGAAGCTGACCTGCAAGTTCAAGTCTACTAGTACGACTGGCGGGTTGACC
TCAGTCTCCTGGAGCTTCCAGCCAGAGGGGGCCGACACTACTGTGTCGTTTTTCCACTACTC
CCAAGGGCAAGTGTACCTTGGGAATTATCCACCATTTAAAGACAGAATCAGCTGGGCTGGAG
ACCTTGACAAGAAAGATGCATCAATCAACATAGAAAATATGCAGTTTATACACAATGGCACC
TATATCTGTGATGTCAAAAACCCTCCTGACATCGTTGTCCAGCCTGGACACATTAGGCTCTA
TGTCGTAGAAAAAGAGAATTTGCCTGTGTTTCCAGTTTGGGTAGTGGTGGGCATAGTTACTG
CTGTGGTCCCTAGGTCTCACTCTGCTCATCAGCATGATTCTGGCTGTCCTCTATAGAAGGAAA
AACTCTAAACGGGATTACACTGGCTGCAGTACATCAGAGAGTTTGTCAACAGTTAAGCAGGC
TCCTCGGAAGTCCCCCTCCGACACTGAGGGTCTTGTAAGAGTCTGCCTTCTGGATCTCACC
AGGGCCCAGTCATATATGCACAGTTAGACCACTCCGGCGGACATCACAGTGACAAGATTAAC
AAGTCAGAGTCTGTGGTGTATGCGGATATCCGAAAGAATTAAGAGAATACCTAGAACATATC
CTCAGCAAGAAACAAAACCAAACCTGGACTCTCGTGCAGAAAATGTAGCCCATTACCACATGT
AGCCTTGGAGACCCAGGCAAGGACAAGTACACGTGTACTCACAGAGGGAGAGAAAGATGTGT
ACAAAGGATATGTATAAATATTCTATTTAGTCATCCTGATATGAGGAGCCAGTGTTGCATGA
TGAAAAGATGGTATGATTCTACATATGTACCCATTGTCTTGCTGTTTTTGTACTTTCTTTTC
AGGTCATTTACAATTGGGAGATTTCAGAAACATTCCTTTCACCATCATTTAGAAATGGTTTG
CCTTAATGGAGACAATAGCAGATCCTGTAGTATTTCCAGTAGACATGGCCTTTTAATCTAAG
GGCTTAAGACTGATTAGTCTTAGCATTTACTGTAGTTGGAGGATGGAGATGCTATGATGGAA
GCATACCCAGGGTGGCCTTTAGCACAGTATCAGTACCATTTATTTGTCTGCCGCTTTTAAAA
AATACCCATTGGCTATGCCACTTGAAAACAATTTGAGAAGTTTTTTTGAAGTTTTTCTCACT
AAAATATGGGGCAATTGTTAGCCTTACATGTTGTGTAGACTTACTTTAAGTTTGCACCCTTG
AAATGTGTCATATCAATTTCTGGATTATAATAGCAAGATTAGCAAAGGATAAATGCCGAAG
GTCACTTCATTCTGGACACAGTTGGATCAATACTGATTAAAGTAGAAAATCCAAGCTTTGCTT
GAGAACTTTTGTAACTGGAGAGTAAAAAGTATCGGTTTTTA

214/270

FIGURE 212

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76510

><subunit 1 of 1, 269 aa, 1 stop

><MW: 29082, pI: 9.02, NX(S/T): 3

MAASAGAGAVIAAPDSRRWLWSVLAAALGLLTAGVSALEVYTPKEIFVANGTQGKLTCKFKS
TSTTGGLTSVSWSFQPEGADTTVSFFHYSQGQVYLGNYPPFKDRISWAGDLDDKKDASINIE
MQFIHNGTYICDVKNPPDIVVQPGHIRLYVVEKENLPVFPVWVVVGIVTAVVLGLTLLISMI
LAVLYRRKNSKRDTGCSLSPVKQAPRKSPDTEGLVKSLPSGSHQGPVIYAQLDHSG
GHHSDKINKSESVVYADIRKN

Signal peptide:

amino acids 1-37

Transmembrane domain:

amino acids 161-183

215/270

FIGURE 213

GCCGGCTGTGCAGAGACGCCATGTACCGGCTCCTGTCAGCAGTGA CTGCCGGGCTGCCGCC
CCCCGGGGCTTGGCCTCAAGCTGCGGACGACGCGGGGTCCATCAGCGCGCCGGGCTGCCGCC
TCTCGGCCACGGCTGGGTGCGGGGCCTCGGGCTGGGGCTGGGGCTGGCGCTCGGGGTGAAGC
TGGCAGGTGGGCTGAGGGGCGCGGCCCCGGCGCAGTCCCCCGCGGCCCCCGACCCTGAGGCG
TCGCCTCTGGCCGAGCCGCCACAGGAGCAGTCCCTCGCCCCGTGGTCTCCGCAGACCCCGGC
GCCGCCCTGCTCCAGGTGCTTCGCCAGAGCCATCGAGAGCAGCCGCGACCTGCTGCACAGGA
TCAAGGATGAGGTGGGCGCACCGGGCATAGTGGTTGGAGTTTCTGTAGATGGAAAAGAAGTC
TGGTCAGAAGGTTTAGGTTATGCTGATGTTGAGAACCGTGTACCATGTAAACCAGAGACAGT
TATGCGAATTGCTAGCATCAGCAAAAGTCTCACCATGGTTGCTCTTGCCAAATTGTGGGAAG
CAGGGAAACTGGATCTTGATATTCCAGTACAACATTATGTTCCCGAATTCCCAGAAAAAGAA
TATGAAGGTGAAAAGGTTTCTGTCACAACAAGATTACTGATTTCCCATTTAAGTGGAATTCG
TCATTATGAAAAGGACATAAAAAAGGTGAAAGAAGAGAAAGCTTATAAAGCCTTGAAGATGA
TGAAAGAGAATGTTGCATTTGAGCAAGAAAAAGAAGGCCAAAAGTAATGAAAAGAATGATTTT
ACTAAATTTAAAACAGAGCAGGAGAATGAAGCCAAATGCCGGAATTCAAAACCTGGCAAGAA
AAAGAATGATTTTGAACAAGGCGAATTATATTTGAGAGAAAAGTTTGAAAATTCAATTGAAT
CCCTAAGATTATTTAAAAATGATCCTTTGTTCTTCAAACCTGGTAGTCAGTTTTTGTATTCA
ACTTTTGGCTATACCCTACTGGCAGCCATAGTAGAGAGAGCTTCAGGATGTAAATATTTGGA
CTATATGCAGAAAATATTCCATGACTTGGATATGCTGACGACTGTGCAGGAAGAAAACGAGC
CAGTGATTTACAATAGAGCAAGGTAAATGAATACCTTCTGCTGTGTCTAGCTATATCGCATC
TTAACACTATTTTATTAATTAAGTCAAATTTTCTTTGTTTCCATTCCAAAATCAACCTGC
CACATTTTGGGAGCTTTTCTACATGTCTGTTTTCTCATCTGTAAAGTGAAGGAAGTAAACA
TGTTTATAAAGTAAAAAAA

FIGURE 214

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76522

><subunit 1 of 1, 373 aa, 1 stop

><MW: 41221, pI: 8.54, NX(S/T): 0

MYRLLSAVTARAAAPGGLASSCGRRGVHQRAGLPPLGHGWVGGLGLGLGLALGVKLAGGLRG
AAPAQSPAAPDPEASPLAEPPEQSLAPWSPQTPAPPCSRCFARAIESSRDLLHRIKDEVGA
PGIVVGVSVDGKEVWSEGLGYADVENRVPCPKPETVMRIASISKSLTMVALAKLWEAGKLDLD
IPVQHYVPEFPEKEYEGEKVSVTTRLLISHLSGIRHYEKDIKKVKEEKAYKALKMMKENVAF
EQEKEGKSNEKNDFTKFKTEQENEAKCRNSKPGKKKNDFEQGELYLREKFENSIESLRLFKN
DPLFFKPGSQFLYSTFGYTLLAAIVERASGCKYLDYMQKIFHDLDMLTTVQEENEPVIYNRAR

Signal peptide:

amino acids 1-19

Transmembrane domain:

amino acids 39-60

FIGURE 215

GTGACACTATAGAAGAGCTATGACGTCGCATGCACGCGTACGTAAGCTCGGAATTCGGCTCG
AGGCTGGTGGGAAGAAGCCGAGATGGCGGCAGCCAGCGCTGGGGCAACCCGGCTGCTCCTGC
TCTTGCTGATGGCGGTAGCAGCGCCCAGTCGAGCCCGGGGCAGCGGCTGCCGGGCCGGGACT
GGTGCGCGAGGGGCTGGGGCGGAAGGTCGAGAGGGCGAGGCCTGTGGCACGGTGGGGCTGCT
GCTGGAGCACTCATTTGAGATCGATGACAGTGCCAACTTCCGGAAGCGGGGCTCACTGCTCT
GGAACCAGCAGGATGGTACCTTGTCCCTGTACAGCGGCAGCTCAGCGAGGAGGAGCGGGGC
CGACTCCGGGATGTGGCAGCCCTGAATGGCCTGTACCGGGTCCGGATCCCAAGGCGACCCGG
GGCCCTGGATGGCCTGGAAGCTGGTGGCTATGTCTCCTCCTTTGTCCCTGCGTGCTCCCTGG
TGGAGTCGCACCTGTCCGACCAGCTGACCCTGCACGTGGATGTGGCCGGCAACGTGGTGGGC
GTGTCGGTGGTGACGCACCCCGGGGGCTGCCGGGGCCATGAGGTGGAGGACGTGGACCTGGA
GCTGTTCAACACCTCGGTGCAGCTGCAGCCGCCACCACAGCCCCAGGCCCTGAGACGGCGG
CCTTCATTGAGCGCCTGGAGATGGAACAGGCCCAGAAGGCCAAGAACCCCCAGGAGCAGAAG
TCCTTCTTCGCCAAATACTGGATGTACATCATTCCCGTCGTCCTGTTCCCTCATGATGTCAGG
AGCGCCAGACACCGGGGGCCAGGGTGGGGGTGGGGGTGGGGGTGGTGGTGGGGGTAGTGGCC
TTTGCTGTGTGCCACCCTCCCTGTAAGTCTATTTAAAAACATCGACGATACATTGAAATGTG
TGAACGTTTTGAAAAGCTACAGCTTCCAGCAGCCAAAAGCAACTGTTGTTTTGGCAAGACGG
TCCTGATGTACAAGCTTGATTGAAATTCAGTCTCACTTGATACGTTATTCAGAAACCCAAG
GAATGGCTGTCCCCATCCTCATGTGGCTGTGTGGAGCTCAGCTGTGTTGTGTGGCAGTTTAT
TAAACTGTCCCCCAGATCGACACGCAAAAAAAAAA

FIGURE 216

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76529

><subunit 1 of 1, 269 aa, 1 stop

><MW: 28004, pI: 5.80, NX(S/T): 1

MAAASAGATRLLLLLLMAVAAPSRARGSGCRAGTGARGAGAEGREGEACGTVGLLLEHSFEI
DDSANFRKRGSLLWNQQDGTLSLSQRQLSEEERGRLRDVAALNGLYRVRI PRRPGALDGLEA
GGYVSSFVPACSLVESHLSDQLTLHVDVAGNVVGVSVVTHPGGCRGHEVEDVDLELFNTSVQ
LQPPTTAPGPETAAFIERLEMEQAQKAKNPQEQKSFFAKYWMYIIPVVLFLMMSGAPDTGGQ
GGGGGGGGGGGSGLCVPPSL

Signal peptide:

amino acids 1-24

Transmembrane domain:

amino acids 226-243

FIGURE 217

GGAGCGCTGCTGGAACCCGAGCCGGAGCCGGAGCCACAGCGGGGAGGGTGGCCTGGCGGCCT
GGAGCCGGACGTGTCCGGGGCGTCCCCGCAGACCGGGGACAGAGGTGTCGGGGGGCCCCACC
ATGCTGGTGA CTGCCTACCTTGCTTTTGTAGGCCTCCTGGCCTCCTGCCTGGGGCTGGA ACT
GTCAAGATGCCGGGCTAAACCCCTGGAAGGGCCTGCAGCAATCCCTCCTTCCTTCGGTTTC
AACTGGACTTCTATCAGGTCTACTTCCTGGCCCTGGCAGCTGATTGGCTTCAGGCCCCCTAC
CTCTATAAACTCTACCAGCATTACTACTTCCTGGAAGGTCAAATTGCCATCCTCTATGTCTG
TGGCCTTGCTCTACAGTCCTCTTTGGCCTAGTGGCCTCCTCCCTTGTTGGATTGGCTGGGTC
GCAAGAATTCTTGTGTCTCTTCTCCCTGACTTACTCACTATGCTGCTTAACCAA ACTCTCT
CAAGACTACTTTGTGCTGCTAGTGGGGCGAGCACTTGGTGGGCTGTCCACAGCCCTGCTCTT
CTCAGCCTTCGAGGCCTGGTATATCCATGAGCACGTGGAACGGCATGACTTCCTGCTGAGT
GGATCCCAGCTACCTTTGCTCGAGCTGCCTTCTGGAACCATGTGCTGGCTGTAGTGGCAGGT
GTGGCAGCTGAGGCTGTAGCCAGCTGGATAGGGCTGGGGCCTGTAGCGCCCTTTGTGGCTGC
CATCCCTCTCCTGGCTCTGGCAGGGGCCTTGGCCCTTCGAAACTGGGGGGAGAACTATGACC
GGCAGCGTGCCTTCTCAAGGACCTGTGCTGGAGGCCTGCGCTGCCTCCTGTGCGACCGCCGC
GTGCTGCTGCTGGGCACCATAACAAGCTCTATTTGAGAGTGTGTCATCTTCATCTTTGTCTTCCT
CTGGACACCTGTGCTGGACCCACACGGGGCCCCCTCTGGGCATTATCTTCTCCAGCTTCATGG
CAGCCAGCCTGCTTGGCTCTTCCCTGTACCGTATCGCCACCTCCAAGAGGTACCACCTTCAG
CCCATGCACCTGCTGTCCCTTGCTGTGCTCATCGTCGTCTTCTCTCTCTTCATGTTGACTTT
CTCTACCAGCCCAGGCCAGGAGAGTCCGGTGGAGTCCTTCATAGCCTTTCTACTTATTGAGT
TGGCTTGTTGGATTATACTTTCCAGCATGAGCTTCCTACGGAGAAAGGTGATCCCTGAGACA
GAGCAGGCTGGTGTACTCAACTGGTTCCGGGTACCTCTGCACTCACTGGCTTGCTAGGGCT
CCTTGTCCTCCATGACAGTGATCGAAAAACAGGCACTCGGAATATGTTACAGATTTGCTCTG
CTGTCATGGTGATGGCTCTGCTGGCAGTGGTGGGACTCTTACCCTGGTAAGGCATGATGCT
GAGCTGCGGGTACCTTCACCTACTGAGGAGCCCTATGCCCCTGAGCTGTAACCCCACTCCAG
GACAAGATAGCTGGGACAGACTCTTGAATTCAGCTATCCGGGATTGTACAGATCTCTCTGT
GACTGACTTTGTGACTGTCTGTGGTTTCTCCTGCCATTGCTTTGTGTTTGGGAGGACATGA
TGGGGGTGATGGACTGGAAAGAAGGTGCCAAAAGTTCCCTCTGTGTTACTCCCATTTAGAAA
ATAAACACTTTTAAATGATCAAAAAAAAAA

FIGURE 218

MLVTAYLAFVGLLASCLGLELSRCRAKPPGRACSNPSFLRFQLDFYQVYFLALAADWLQAPY
LYKLYQHYYFLEGQIAILYVCGLASTVLFGLVASSLVDWLGRKNSCVLFSLTYSLCCLTKLS
QDYFVLLVGRALGGLSTALLFSAFEAWYIHEHVERHDFPAEWIPATFARAAFWNHVLAVVAG
VAAEAVASWIGLGPVAPFVAAIPLLALAGALALRNWGENYDRQRAFSTRCAGGLRCLLSDRR
VLLLGTIQALFESVIFIFVFLWTPVLDPHGAPLGIIFSSFMAASLLGSSLYRIATSKRYHLQ
PMHLLSLAVLIVVFSLFMLTFSTSPGQESPVESFIAFLLIELACGLYFSPMSFLRRKVIPET
EQAGVLNWFRVPLHSLACLGLLVLHDSRKTGTRNMFSCSAVMVMALLAVVGLFTVVVRHDA
ELRVPSPTTEEPYAPEL

Signal peptide:

amino acids 1-18

Transmembrane domain:amino acids 41-55, 75-94, 127-143, 191-213, 249-270, 278-299,
314-330, 343-359, 379-394, 410-430

FIGURE 219

GCGACGCGCGGCGGGGCGGCGAGAGGAAACGCGGCGCCGGGCGGGCCCGGCCCTGGAGATG
GTCCCCGGCGCCGCGGGCTGGTGTGTCTCGTGCTCTGGCTCCCCGCGTGCGTCGCGGCCCA
CGGCTTCCGTATCCATGATTATTTGTACTTTCAAGTGCTGAGTCCTGGGGACATTCGATACA
TCTTCACAGCCACACCTGCCAAGGACTTTGGTGGTATCTTTCACACAAGGTATGAGCAGATT
CACCTTGTCCCCGCTGAACCTCCAGAGGCCTGCGGGGAACTCAGCAACGGTTTCTTCATCCA
GGACCAGATTGCTCTGGTGGAGAGGGGGGGCTGCTCCTTCCTCTCCAAGACTCGGGTGGTCC
AGGAGCACGGCGGGCGGGCGGTGATCATCTCTGACAACGCAGTTGACAATGACAGCTTCTAC
GTGGAGATGATCCAGGACAGTACCCAGCGCACAGCTGACATCCCCGCCCTCTTCCTGCTCGG
CCGAGACGGCTACATGATCCGCCGCTCTCTGGAACAGCATGGGCTGCCATGGGCCATCATTT
CCATCCCAGTCAATGTCACCAGCATCCCCACCTTTGAGCTGCTGCAACCGCCCTGGACCTTC
TGGTAGAAAGAGTTTGTCCACATTCCAGCCATAAGTGACTCTGAGCTGGGAAGGGGAAACCC
AGGAATTTTGCTACTTGGAATTTGGAGATAGCATCTGGGGACAAGTGGAGCCAGGTAGAGGA
AAAGGGTTTGGGCGTTGCTAGGCTGAAAGGGAAGCCACACCACTGGCCTTCCCTTCCCCAGG
GCCCCCAAGGGTGTCTCATGCTACAAGAAGAGGCAAGAGACAGGCCCCAGGGCTTCTGGCTA
GAACCCGAAACAAAAGGAGCTGAAGGCAGGTGGCCTGAGAGCCATCTGTGACCTGTCACACT
CACCTGGCTCCAGCCTCCCCTACCCAGGGTCTCTGCACAGTGACCTTCACAGCAGTTGTTGG
AGTGGTTTAAAGAGCTGGTGTTTGGGGACTCAATAAACCCCTCACTGACTTTTTAGCAATAAA
GCTTCTCATCAGGGTTGCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 220

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76532

><subunit 1 of 1, 188 aa, 1 stop

><MW: 21042, pI: 5.36, NX(S/T): 2

MVPGAAGWCCLVLWLPACVAAHGFRIDYLYFQVLSPGDIRYIFTATPAKDFGGIFHTRYEQ

IHLVPAEPPEACGELSNGFFIQDQIALVERGGCSFLSKTRVVQEHGGRAVIISDNAVDNDSF

YVEMIQDSTQRTADIPALFLLGRDGYMIRRSLEQHGLPWAIISIPVNVTSIPTFELLQPPWTFW

Signal peptide:

amino acids 1-20

FIGURE 221

TCTGCCTCCACTGCTCTGTGCTGGGATCATGGAACTTGCACTGCTGTGTGGGCTGGTGGTGA
TGGCTGGTGTGATTCCAATCCAGGGCGGGATCCTGAACCTGAACAAGATGGTCAAGCAAGTG
ACTGGGAAAATGCCCATCCTCTCCTACTGGCCCTACGGCTGTCACTGCGGACTAGGTGGCAG
AGGCCAACCCAAAGATGCCACGGACTGGTGCTGCCAGACCCATGACTGCTGCTATGACCACC
TGAAGACCCAGGGGTGCGGCATCTACAAGGACAACAACAAAAGCAGCATACATTGTATGGAT
TTATCTCAACGCTATTGTTTAATGGCTGTGTTTAATGTGATCTATCTGGAAAATGAGGACTC
CGAATAAAAAGCTATTACTAWTTNAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
AA

FIGURE 222

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76538

><subunit 1 of 1, 116 aa, 1 stop

><MW: 12910, pI: 6.41, NX(S/T): 1

MELALLCGLVVMAGVPIQGGILNLNKMVKQVTGKMPILSYWPYGCHCGLGGRGQPKDATDW
CCQTHDCCYDHLKTQGCgiYKDNNKSSIHCMdLSQRYCLMAVFNViiYLENEDESE

Important features of the protein:

Signal peptide:

amino acids 1-17

Transmembrane domain:

amino acids 1-24

N-glycosylation site.

amino acids 86-89

N-myristoylation sites.

amino acids 20-25, 45-50

Phospholipase A2 histidine active site.

amino acids 63-70

FIGURE 223

CTCGCTTCTTCCTTCTGGATGGGGGGCCCAGGGGGCCCAGGAGAGTATAAAGGCGATGTGGAG
GGTGCCCGGCACAACCAGACGCCCAGTCACAGGCGAGAGCCCTGGGATGCACCGGCCAGAGG
CCATGCTGCTGCTGCTCACGCTTGCCCTCCTGGGGGGGGCCCCACCTGGGCAGGGAAGATGTAT
GGCCCTGGAGGAGGCAAGTATTTTCAGCACCACTGAAGACTACGACCATGAAATCACAGGGCT
GCGGGTGTCTGTAGGTCTTCTCCTGGTGAAAAGTGTCCAGGTGAAACTTGAGACTCCTGGG
ACGTGAAACTGGGAGCCTTAGGTGGGAATACCCAGGAAGTCACCCTGCAGCCAGGCGAATAC
ATCACAAAAGTCTTTGTCGCCTTCCAAGCTTTCCTCCGGGGTATGGTCATGTACACCAGCAA
GGACCGCTATTTCTATTTTGGAAGCTTGATGGCCAGATCTCCTCTGCCTACCCAGCCAAG
AGGGGCAGGTGCTGGTGGGCATCTATGGCCAGTATCAACTCCTTGGCATCAAGAGCATTGGC
TTTGAATGGAATTATCCACTAGAGGAGCCGACCACTGAGCCACCAGTTAATCTCACATACTC
AGCAAACCTCACCCGTGGGTCGCTAGGGTGGGGTATGGGGCCATCCGAGCTGAGGCCATCTGT
GTGGTGGTGGCTGATGGTACTGGAGTAACTGAGTCGGGACGCTGAATCTGAATCCACCAATA
AATAAAGCTTCTGCGAGAAAA

FIGURE 224

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76541

><subunit 1 of 1, 178 aa, 1 stop

><MW: 19600, pI: 5.89, NX(S/T): 1

MHRPEAMLLLLTLALLGGPTWAGKMYGPGGGKYFSTTEDYDHEITGLRVSVGLLLVKSVQVK
LGDSWDVKLGALGGNTQEVTLQPGYITKVFVAFQAFLRGMVMYTSKDRYFYFGKLDGQISS
AYPSQEGQVLVGIYGQYQLLGIKSIGFEWNYPLEEPTTEPPVNLTYSANSPVGR

Signal peptide:

amino acids 1-22

FIGURE 225

GCTGAGCGTGTGCGCGGTACGGGGCTCTCCTGCCTTCTGGGCTCCAACGCAGCTCTGTGGCT
GAACTGGGTGCTCATCACGGGAAGTCTGGGCTATGGAATACAGATGTGGCAGCTCAGGTAG
CCCCAAATTGCCTGGAAGAATACATCATGTTTTTCGATAAGAAGAAATTGTAGGATCCAGTT
TTTTTTTTTAACCGCCCCCTCCCCACCCCCCAAAAAAAGTGTAAAGATGCAAAAACGTAATAT
CCATGAAGATCCTATTACCTAGGAAGATTTTGATGTTTTGCTGCGAATGCGGTGTTGGGATT
TATTTGTTCTTGGAGTGTTCTGCGTGGCTGGCAAAGAATAATGTTCCAAAATCGGTCCATCT
CCCAAGGGGTCCAATTTTTCTTCTGGGTGTGAGCGAGCCCTGACTCACTACAGTGCAGCTG
ACAGGGGCTGTGATGCAACTGGCCCCCTAAGCCAAAGCAAAGACCTAAGGACGACCTTTGAA
CAATACAAAGGATGGGTTTCAATGTAATTAGGCTACTGAGCGGATCAGCTGTAGCACTGGTT
ATAGCCCCCACTGTCTTACTGACAATGCTTTCTTCTGCCGAACGAGGATGCCCTAAGGGCTG
TAGGTGTGAAGGCAAAATGGTATATTGTGAATCTCAGAAATTACAGGAGATACCCCTCAAGTA
TATCTGCTGGTTGCTTAGGTTTGTCCCTTCGCTATAACAGCCTTCAAAAAGCTTAAGTATAAT
CAATTTAAAGGGCTCAACCAGCTCACCTGGCTATACCTTGACCATAACCATATCAGCAATAT
TGACGAAAATGCTTTTAATGGAATACGCAGACTCAAAGAGCTGATTCTTAGTTCCAATAGAA
TCTCCTATTTTCTTAACAATACCTTCAGACCTGTGACAAATTTACGGAACCTGGATCTGTCC
TATAATCAGCTGCATTCTCTGGGATCTGAACAGTTTCGGGGCTTGCGGAAGCTGCTGAGTTT
ACATTTACGGTCTAACTCCCTGAGAACCATCCCTGTGCGAATATTCCAAGACTGCCGCAACC
TGGAACCTTTTGGACCTGGGATATAACCGGATCCGAAGTTTAGCCAGGAATGTCTTTGCTGGC
ATGATCAGACTCAAAGAACTTCACCTGGAGCACAATCAATTTTCCAAGCTCAACCTGGCCCT
TTTTCCAAGGTTGGTCAGCCTTCAGAACCTTTACTTGCAAGTGAATAAAATCAGTGTATAG
GACAGACCATGTCTGGACCTGGAGCTCCTTACAAAGGCTTGATTTATCAGGCAATGAGATC
GAAGCTTTCAGTGGACCCAGTGTTTTCCAGTGTGTCCCGAATCTGCAGCGCCTCAACCTGGA
TTCCAACAAGCTCACATTTATTGGTCAAGAGATTTTGGATTCTTGGATATCCCTCAATGACA
TCAGTCTTGCTGGGAATATATGGGAATGCAGCAGAAATATTGCTCCCTTGTAAGCTGGCTG
AAAAGTTTTAAAGGTCTAAGGGAGAATACAATTATCTGTGCCAGTCCCAAAGAGCTGCAAGG
AGTAAATGTGATCGATGCAGTGAAGAACTACAGCATCTGTGGCAAAAGTACTACAGAGAGGT
TTGATCTGGCCAGGGCTCTCCCAAAGCCGACGTTTAAGCCCAAGCTCCCCAGGCCGAAGCAT
GAGAGCAAACCCCTTTGCCCCCGACGGTGGGAGCCACAGAGCCCGGCCAGAGACCGATGC
TGACGCCGAGCACATCTCTTCCATAAAATCATCGCGGGCAGCGTGGCGCTTTTCTGTCCG
TGCTCGTCATCCTGCTGGTTATCTACGTGTCATGGAAGCGGTACCCTGCGAGCATGAAGCAG
CTGCAGCAGCGCTCCCTCATGCGAAGGCACAGGAAAAAGAAAAGACAGTCCCTAAAGCAAAT
GACTCCCAGCACCCAGGAATTTTATGTAGATTATAAACCCACCAACACGGAGACCAGCGAGA
TGCTGCTGAATGGGACGGGACCCTGCACCTATAACAAATCGGGCTCCAGGGAGTGTGAGGTA
TGAACCATTGTGATAAAAAAGAGCTCTTAAAGCTGGGAAATAAGTGGTGCTTTATTGAACTC
TGGTGACTATCAAGGGAACGCGATGCCCCCCTCCCTTCCCTCTCCCTCTCACTTTGGTG
CAAGATCCTTCCTTGTCGTTTTAGTGCATTTCATAATACTGGTCATTTTCTCTCATACATA
ATCAACCCATTGAAATTTAAATACCACAATCAATGTGAAGCTTGAACCTCCGGTTTAAATATA
TACCTATTGTATAAGACCCTTTACTGATTCCATTAATGTCGCATTTGTTTTAAGATAAAACT
TCTTTCATAGGTAAAAA

FIGURE 226

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77301

><subunit 1 of 1, 513 aa, 1 stop

><MW: 58266, pI: 9.84, NX(S/T): 4

MGFNVIRLLSGSAVALVIAPTVELLTMSSAERGCPKGCRCEGKMVYCESQKLQEIPSSISAG
CLGLSLRYNSLQKLKYNQFKGLNQLTWLYLDHNNHISNIDENAFNGIRRLKELILSSNRISYF
LNNTFRPVTNLRNLDLSYNQLHSLGSEQFRGLRKLLSLHLRSNSLRITIPVRIFQDCRNLELL
DLGYNRIRSLARNVFAFMIRLKEHLHLEHNQFSKLNALFPRLVSLQNLQWNLKISVIGQTM
SWTWSSLQRLDLSGNEIEAFSGPSVFQCVPNLQRLNLDNKLTFIGQEILDSWISLNDISLA
GNIWECSRNICSLVNWLKSFKGLRENTIICASPKEQGVNVIDAVKNYSICGKSTTERFDLA
RALPKPTFKPKLPRPKHESKPPLPPTVGATEPGPETDADAEHISFHKIIAGSVALFLSVLVI
LLVIYVSWKRYPASMKQLQQRSLMRRHRKKKRQSLKQMTPTSTQEFYVDYKPTNTTETSEMLLN
GTGPCTYNKSGSRECEV

Important features of the protein:

Signal peptide:

amino acids 1-33

Transmembrane domain:

amino acids 420-442

N-glycosylation sites.

amino acids 126-129, 357-360, 496-499, 504-507

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 465-468

Tyrosine kinase phosphorylation site.

amino acids 136-142

N-myristoylation sites.

amino acids 11-16, 33-38, 245-250, 332-337, 497-502, 507-512

229/270

FIGURE 227

AGTTCTGAGAAAGAAGGAAATAAACACAGGCACCAAACCACTATCCTAAGTTGACTGTCCTT
TAAATATGTCAAGATCCAGACTTTTCAGTGTACCTCAGCGATCTCAACGATAGGGATCTTG
TGTTTGCCGCTATTCCAGTTGGTGCTCTCGGACCTACCATGCGAAGAAGATGAAATGTGTGT
AAATTATAATGACCAACACCCTAATGGCTGGTATATCTGGATCCTCCTGCTGCTGGTTTTTG
TGGCAGCTCTTCTCTGTGGAGCTGTGGTCCTCTGCCTCCAGTGCTGGCTGAGGAGACCCCGA
ATTGATTCTCACAGGCGCACCATGGCAGTTTTTGTCTGTTGGAGACTTGGACTCTATTTATGG
GACAGAAGCAGCTGTGAGTCCAAGTGTGGAAATTCACCTTCAAACCTCAAACCCCTGACCTAT
ATCCTGTTCTGCTCCATGTTTTTGGCCCTTTAGGCTCCCCACCTCCATATGAAGAAATTGTA
AAAACAACCTTGATTTTAGGTGTGGATTATCAATTTAAAGTATTAACGACATCTGTAATTCCA
AAACATCAAATTTAGGAATAGTTATTTTCAGTTGTTGGAAATGTCCAGAGATCTATTCATATA
GTCTGAGGAAGGACAATTCGACAAAAGAATGGATGTTGGAAAAAATTTTGGTCATGGAGATG
TTTAAATAGTAAAGTAGCAGGCTTTTGATGTGTCACTGCTGTATCATACTTTTATGCTACAC
AACCAAATTAATGCTTCTCCACTAGTATCCAAACAGGCAACAATTAGGTGCTGGAAGTAGTT
TCCATCACATTTAGGACTCCACTGCAGTATACAGCACACCATTTTCTGCTTTAAACTCTTTC
CTAGCATGGGGTCCATAAAAATTATTATAATTTAACAATAGCCCAAGCCGAGAATCCAACAT
GTCCAGAACCAGAACCAGAAAGATAGTATTTGAATGAAGGTGAGGGGAGAGAGTAGGAAAAA
GAAAAGTTTGGAGTTGAAGGGTAAAGGATAAATGAAGAGGAAAAGGAAAAGATTACAAGTCT
CAGCAAAAACAAGAGGTTTTATGCCCAACCTGAAGAGGAAGAAATTGTAGATAGAAGGTGA
AGGAGATTGCTGAAGATATAGAGCATATAATGCCAACACGGGGAGAAAAGAAAATTTCCC
CTTTTACAGTAATGAATGTGGCCTCCATAGTCCATAGTGTCTCTGGAGCCTCAGGGCTTG
GCATTTATTGCAGCATCATGCTAAGAACCTTCGGCATAGGTATCTGTTCCCATGAGGACTGC
AGAAGTAGCAATGAGACATCTTCAAGTGGCATTTTGGCAGTGGCCATCAGCAGGGGGACAGA
CAAAAACATCCATCACAGATGACATATGATCTTCAGCTGACAAATTTGTTGAACAAAACAAT
AAACATCAATAGATATCTAAAAA

FIGURE 228

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77303

><subunit 1 of 1, 146 aa, 1 stop

><MW: 16116, pI: 4.99, NX(S/T): 0

MSRSRLFSVTSAISTIGILCLPLFQLVLSDLPCCEEDEMCVNYNDQHPNGWYIWILLLLVLVA
ALLCGAVVLCLQCWLRRPRIDSHRRTMAVFAVGDLDSIYGTEAAVSPTVGIHLQTQTPDLYP
VPAPCFGPLGSPPPYEEIVKTT

Signal peptide:

amino acids 1-29

Transmembrane domain:

amino acids 52-70

FIGURE 229

GAGCGGAGTAAATCTCCACAAGCTGGGAACAAACCTCGTCCCAACTCCCACCCACCGGCGT
TTCTCCAGCTCGATCTGGAGGCTGCTTCGCCAGTGTGGGACGCAGCTGACGCCCCGCTTATTA
GCTCTCGCTGCGTCGCCCCGGCTCAGAAGCTCCGTGGCGGGCGGCGACCGTGACGAGAAGCCC
ACGGCCAGCTCAGTTCTCTTCTACTTTGGGAGAGAGAGAAAGTCAGATGCCCCCTTTTAAACT
CCCTCTTCAAAACTCATCTCCTGGGTGACTGAGTTAATAGAGTGGATACAACCTTGCTGAAG
ATGAAGAATATACAATATTGAGGATATTTTTTCTTTTTTTTTCAAGTCTTGATTTGTGGC
TTACCTCAAGTTACCATTTTTTCAAGTCAAGTCTGTTTGTGTTGCTTCTTCAGAAATGTTTTTA
CAATCTCAAGAAAAAATATGTCCCAGAAATTGAGTTTACTGTTGCTTGTATTGGAATCATT
TGGGGATTGATGTTACTGCACTATACTTTTCAACAACCAAGACATCAAAGCAGTGTCAAGTT
ACGTGAGCAAATACTAGACTTAAGCAAAAGATATGTTAAAGCTCTAGCAGAGGAAAATAAGA
ACACAGTGGATGTGAGAACGGTGCTTCTATGGCAGGATATGCGGATCTGAAAAGAACAATT
GCTGTCCTTCTGGATGACATTTTGCAACGATTGGTGAAGCTGGAGAACAAAGTTGACTATAT
TGTTGTGAATGGCTCAGCAGCCAACACCACCAATGGTACTAGTGGGAATTTGGTGCCAGTAA
CCACAAATAAAAGAACGAATGTCTCGGGCAGTATCAGATAGCAGTTGAAAATCACTTGTGC
TGCTCCATCCACTGTGGATTATATCCTATGGCAGAAAAGCTTTATAATTGCTGGCTTAGGAC
AGAGCAATACTTTACAATAAAAGCTCTACACATTTTCAAGGAGTATGCTGGATTCATGGAAC
TCTAATTCTGTACATAAAAATTTTAAAGTTATTTGTTTGCTTTCAGGCAAGTCTGTTCAATG
CTGTACTATGTCCTTAAAGAGAATTTGGTAACTTGGTTGATGTGGTAAGCAGATAGGTGAGT
TTTGATATAAATCTTTTGTGTTTGAAGTCAAGCTGAAATGAAAACACTGAAAAACATGGATT
ATTTCTATAACACATTTATTTAAGTATATAACACGTTTTTTTGGACAAGTGAAGAATGTTTAA
TCATTCTGTCATTTGTTCTCAATAGATGTAAGTGTAGACTACGGCTATTTGAAAAAATGTG
CTTATTGTACTATATTTTGTATTCCAATTATGAGCAGAGAAAGGAAATATAATGTTGAAAA
TAATGTTTTGAAATCATGACCCAAAGAATGTATTGATTGCACTATCCTTCAGAATAACTGA
AGGTTAATTATTGTATATTTTTTAAAAATTACACTTATAAGAGTATAATCTTGAAATGGGTAG
CAGCCACTGTCCATTACCTATCGTAAACATTGGGGCAATTTAATAACAGCATTTAAATAGTT
GTAAACTCTAATCTTATACTTATTGAAGAATAAAAGATATTTTTATGATGAGAGTAACAATA
AAGTATTCATGATTTTTTACATACATGAATGTTTCAATTTAAAAGTTTAACTCTTGAGTGTCT
ATGCTATCAGGAAAGCACATTATTTCCATATTTGGGTAAATTTTGCTTTTATTATATTGGTC
TAGGAGGAAGGGACTTTGGAGAATGGAACCTCTGAGGACTTTAGCCAGGTGTATATAATAAA
GGTACTTTTGTGCTGCATTAAATTGCTTGGAAGTGTTAACATTATATTATAAAGAGTATC
CTTTATGAAATTTTGAATTTGTATAACAGATGCATTAGATATTCATTTTATATAATGGCCAC
TTAAATAAGAACATTTAAATATAAACTATGAAGATTGACTATCTTTTCAGGAAAAAGCT
GTATATAGCACAGGGAACCCTAATCTTGGGTAATTCTAGTATAAAACAAATTATACTTTTAT
TTAAATTTCCCTTGTAGCAAATCTAATTGCCACATGGTGCCCTATATTTTCATAGTATTTATT
CTCTATAGTAACTGCTTAAGTGCAGCTAGCTTCTAGATTTAGACTATATAGAATTTAGATAT
TGTATTGTTTCGTCATTATAATATGCTACCACATGTAGCAATAATTACAATATTTTATTAATA
TAAATATGTGAAATATTGTTTCATGAAAGACAGATTTCCAAATCTCTCTTCTCTCTCTGTA
CTGTCTACCTTTATGTGAAGAAATTAATTATATGCCATTGCCAGGT

FIGURE 230

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77648

><subunit 1 of 1, 140 aa, 1 stop

><MW: 15668, pI: 10.14, NX(S/T): 5

MFFTISRKNMSQKLSLLLLVFGLIWGLMLLHYTFQQPRHQSSVKLREQILDLSKRYVKALAE

ENKNTVDVENGASMAGYADLKRTIAVLLDDILQRLVKLENKVDYIVVNGSAANTTNGTSGNL

VPVTTNKRTNVSGSIR

Important features of the protein:

Signal peptide:

amino acids 1-26

FIGURE 231

CGCGGCCGGGCCCGCCGGGGTGAGCGTGCCGAGGCGGCTGTGGCGCAGGCTTCCAGCCCCAC
CATGCCGTGGCCCCCTGCTGCTGCTGCTGGCCGTGAGTGGGGCCAGACAACCCGGCCATGCT
TCCCCGGGTGCCAATGCGAGGTGGAGACCTTCGGCCTTTTCGACAGCTTCAGCCTGACTCGG
GTGGATTGTAGCGGCCTGGGCCCCACATCATGCCGGTGCCCATCCCTCTGGACACAGCCCA
CTTGACCTGTCTCCAACCGGCTGGAGATGGTGAATGAGTCGGTGTTGGCGGGGCCGGGCT
ACACGACGTTGGCTGGCCTGGATCTCAGCCACAACCTGCTCACCAGCATCTCACCCACTGCC
TTCTCCCGCCTTCGCTACCTGGAGTCGCTTGACCTCAGCCACAATGGCCTGACAGCCCTGCC
AGCCGAGAGCTTCACCAGCTCACCCCTGAGCGACGTGAACCTTAGCCACAACCAGCTCCGGG
AGGTCTCAGTGTCTGCCTTCACGACGCACAGTCAGGGCCGGGCACTACACGTGGACCTCTCC
CACAACCTCATTACCGCCTCGTGCCCCACCCACGAGGGCCGGCCTGCCTGCGCCCAACAT
TCAGAGCCTGAACCTGGCCTGGAACCGGCTCCATGCCGTGCCCAACCTCCGAGACTTGCCCC
TGCGCTACCTGAGCCTGGATGGGAACCCCTCTAGCTGTCAATTGGTCCGGGTGCCTTCGCGGGG
CTGGGAGGCCCTTACACACCTGTCTCTGGCCAGCCTGCAGAGGCTCCCTGAGCTGGCGCCAG
TGGCTTCCGTGAGCTACCGGGCCTGCAGGTCCTGGACCTGTGGGCAACCCCAAGCTTAAT
GGGACAGGAGCTGAGGTGTTTTAGGCCTGAGCTCCCTGCAGGAGCTGGACCTTTCCGGCACC
AACCTGGTGGCCCTGCCTGAGGCGCTGCTCCTCCACCTCCCGGCACTGCAGAGCGTCAGCGT
GGGCCAGGATGTGCGGTGCCGGCGCCTGGTGCGGGAGGGCACCTACCCCCGAGGCCTGGCT
CCAGCCCCAAGGTGCCCCCTGCACTGCGTAGACACCCGGGAATCTGCTGCCAGGGGCCCCACC
ATCTTGTGACAAATGGTGTGGCCAGGGCCACATAACAGACTGCTGTCTTGGGCTGCCTCAG
GTCCCGAGTAACTTATGTTCAATGTGCCAACACCAGTGGGGAGCCCGCAGGCCTATGTGGCA
GCGTCACCACAGGAGTTGTGGGCCTAGGAGAGGCTTTGGACCTGGGAGCCACACCTAGGAGC
AAAGTCTACCCCTTTGTCTACGTTGCTTCCCCAAACCATGAGCAGAGGGACTTCGATGCCA
AACCAGACTCGGGTCCCCCTCCTGCTTCCCTTCCCCACTTATCCCCCAAGTGCCTTCCCTCAT
GCCTGGGGCCGGCCTGACCCGCAATGGGCAGAGGGTGGGTGGGACCCCTGCTGCAGGGCAGA
GTTACAGGTCCACTGGGCTGAGTGTCCCCTTGGGCCCATGGCCAGTCACTCAGGGGCGAGTT
TCTTTTCTAACATAGCCCTTTCTTTGCCATGAGGCCATGAGGCCCGCTTCATCCTTTTCTAT
TTCCCTAGAACCTTAATGGTAGAAGGAATTGCAAAGAATCAAGTCCACCCCTTCTCATGTGAC
AGATGGGGAACTGAGGCCTTGAGAAGGAAAAAGGCTAATCTAAGTTCCTGCGGGCAGTGGC
ATGACTGGAGCACAGCCTCCTGCCTCCAGCCCGGACCCAATGCACTTTCTTGTCTCCTCTA
ATAAGCCCCACCCTCCCCGCCTGGGCTCCCCTTGCTGCCCTTGCTGTTCCCCATTAGCACA
GGAGTAGCAGCAGCAGGACAGGCAAGAGCCTCACAAGTGGGACTCTGGGCCTCTGACCAGCT
GTGCGGCATGGGCTAAGTCACTCTGCCCTTCGGAGCCTCTGGAAGCTTAGGGCACATTGGTT
CCAGCCTAGCCAGTTTCTCACCCCTGGGTGGGGTCCCCAGCATCCAGACTGGAAACCTACC
CATTTTCCCTGAGCATCCTCTAGATGCTGCCCAAGGAGTTGCTGCAGTTCTGGAGCCTCA
TCTGGCTGGGATCTCCAAGGGGCTCCTGGATTAGTCCCCACTGGCCCTGAGCACGACAGC
CCTTCTTACCCTCCCAGGAATGCCGTGAAAGGAGACAAGGTCTGCCCCGACCCATGTCTATGC
TCTACCCCCAGGGCAGCATCTCAGCTTCCGAACCCCTGGGCTGTTTCCTTAGTCTTCATTTTA
TAAAAGTTGTTGCCTTTTAAACGGAGTGTCACTTTCAACCGGCCTCCCCTACCCCTGCTGGC
CGGGGATGGAGACATGTCAATTTGTAAAAGCAGAAAAAGGTTGCATTTGTTCACTTTTGTAAAT
ATTGTCCTGGGCCTGTGTTGGGGTGTGGGGGAAGCTGGGCATCAGTGGCCACATGGGCATC
AGGGGCTGGCCCCACAGAGACCCACAGGGCAGTGAGCTCTGTCTTCCCCACCTGCCTAGC
CCATCATCTATCTAACCGGTCTTGATTTAATAAACACTATAAAAGGTTTAAAAAAAAAAAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 232

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77652

><subunit 1 of 1, 353 aa, 1 stop

><MW: 37847, pI: 6.80, NX(S/T): 2

MPWPLLLLLLAVSGAQTTTRPCFPGCQCEVETFGLFDSFSLTRVDCSGLGPHIMPVPIPLDTAH
LDLSSNRLEMVNESVLAGPGYTTLAGLDLSHNLLTSISPTAFSRLRYLESLDLSHNGLTALP
AESFTSSPLSDVNLSHNQLREVSVSFAFTTHSQGRALHVDLSHNLIHRLVPHPTRAGLPAPTI
QSLNLAWNRLHAVPNLRDLPLRYLSLDGNPLAVIGPGAFAGLGGLTHLSLASLQRLPELAPS
GFRELPGQLQVLDLSGNPKLNWAGAEVFSGLSSLQELDLSGTNLVPLPEALLHLPALQSVSV
GQDVRCRRLVREGTYPRRPGSSPKVPLHCVDTRESAARGPTIL

Signal peptide:

amino acids 1-16

Transmembrane domains:

amino acids 215-232, 287-304

FIGURE 233

GATGGCGCAGCCACAGCTTCTGTGAGATTGATTTCTCCCCAGTTCCCCTGTGGGTCTGAGG
GGACCAGAAGGGTGAGCTACGTTGGCTTTCTGGAAGGGGAGGCTATATGCGTCAATTCCCCA
AAACAAGTTTTGACATTTCCCCTGAAATGTCATTCTCTATCTATTCACTGCAAGTGCCTGCT
GTTCCAGGCCTTACCTGCTGGGCACTAACGGCGGAGCCAGGATGGGGACAGAATAAAGGAGC
CACGACCTGTGCCACCAACTCGCACTCAGACTCTGAACTCAGACCTGAAATCTTCTCTTCAC
GGGAGGCTTGGCAGTTTTTCTTACTCCTGTGGTCTCCAGATTTAGGCCTAAGATGAAAGCC
TCTAGTCTTGCCTTCAGCCTTCTCTCTGCTGCGTTTTATCTCCTATGGACTCCTTCCACTGG
ACTGAAGACACTCAATTTGGGAAGCTGTGTGATCGCCACAAACCTTCAGGAAATACGAAATG
GATTTTCTGAGATACGGGGCAGTGTGCAAGCCAAAGATGGAAACATTGACATCAGAATCTTA
AGGAGGACTGAGTCTTTGCAAGACACAAAGCCTGCGAATCGATGCTGCCTCCTGCGCCATTT
GCTAAGACTCTATCTGGACAGGGTATTTAAAAACTACCAGACCCCTGACCATTATACTCTCC
GGAAGATCAGCAGCCTCGCCAATTCCTTTCTTACCATCAAGAAGGACCTCCGGCTCTCTCAT
GCCCACATGACATGCCATTGTGGGGAGGAAGCAATGAAGAAATACAGCCAGATTCTGAGTCA
CTTTGAAAAGCTGGAACCTCAGGCAGCAGTTGTGAAGGCTTTGGGGGAACTAGACATTCTTC
TGCAATGGATGGAGGAGACAGAATAGGAGGAAAGTGATGCTGCTGCTAAGAATATTCGAGGT
CAAGAGCTCCAGTCTTCAATACCTGCAGAGGAGGCATGACCCCAAACCACCATCTCTTTACT
GTACTAGTCTTGTGCTGGTCACAGTGTATCTTATTTATGCATTACTTGCTTCCTTGCATGAT
TGTCTTTATGCATCCCCAATCTTAATTGAGACCATACTTGTATAAGATTTTTGTAATATCTT
TCTGCTATTGGATATATTTATTAGTTAATATATTTATTTATTTTTTGCTATTTAATGTATTT
ATTTTTTTACTTGGACATGAACTTTAAAAAAATTCACAGATTATATTTATAACCTGACTAG
AGCAGGTGATGTATTTTTTATACAGTAAAAAATAACCTTGTAATTCTAGAAGAGTGGCT
AGGGGGGTATTCAATTTGTATTCAACTAAGGACATATTTACTCATGCTGATGCTCTGTGAGA
TATTTGAAATTGAACCAATGACTACTTAGGATGGGTTGTGGAATAAGTTTTGATGTGGAATT
GCACATCTACCTTACAATTACTGACCATCCCCAGTAGACTCCCCAGTCCCATAATTGTGTAT
CTTCCAGCCAGGAATCCTACACGGCCAGCATGTATTTCTACAAATAAAGTTTTCTTTGCATA
CCAAAAAAAAAAAAAAAAAAAA

FIGURE 234

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA83500

><subunit 1 of 1, 261 aa, 1 stop

><MW: 29667, pI: 8.76, NX(S/T): 0

MRQFPKTSFDISPEMSFSIYSLQVPAVPGLTCWALTAEPGWGQNKGATTCATNSHSDSELRP
EIFSSREAWQFFLLWSPDFRPKMKASSLAFSLLSAAFYLLWTPSTGLKTLNLGSCVIATNL
QEIRNGFSEIRGSVQAKDGNIDIRILRRTESLQDTKPANRCCLLRHLLRLYLDRVFKNYQTP
DHYTLRKISSLANSTLTIKKDLRLSHAHMTCHCGEEAMKKYSQILSHFEKLEPQAAVVKALG
ELDILLQWMEETE

Important features of the protein:

Signal peptide:

amino acids 1-42

cAMP- and cGMP-dependent protein kinase phosphorylation sites.

amino acids 192-195, 225-228

N-myristoylation sites.

amino acids 42-47, 46-51, 136-141

FIGURE 235

CCGTTATCGTCTTGCGCTACTGCTGAATGTCCGTCCCGGAGGAGGAGAGAGGCTTTTGCCG
CTGACCCAGAGATGGCCCCGAGCGAGCAAATTCCTACTGTCCGGCTGCGCGGCTACCGTGGC
CGAGCTAGCAACCTTTCCCCTGGATCTCACAAAACTCGACTCCAAATGCAAGGAGAAGCAG
CTCTTGCTCGGTGGGAGACGGTGCAAGAGAATCTGCCCCCTATAGGGGAATGGTGCGCACA
GCCCTAGGGATCATTGAAGAGGAAGGCTTTCTAAAGCTTTGGCAAGGAGTGACACCCGCCAT
TTACAGACACGTAGTGTATTCTGGAGGTCGAATGGTCACATATGAACATCTCCGAGAGGTTG
TGTTTGGCAAAAGTGAAGATGAGCATTATCCCCTTTGGAAATCAGTCATTGGAGGGATGATG
GCTGGTGTTATTGGCCAGTTTTTTAGCCAATCCAAGTACCTAGTGAAGGTTTCAGATGCAAAT
GGAAGGAAAAAGGAACTGGAAGGAAAACCATTCGCGATTTCTGTGGTGTACATCATGCATTTG
CAAAAATCTTAGCTGAAGGAGGAATACGAGGGCTTTGGGCAGGCTGGGTACCCAATATACAA
AGAGCAGCACTGGTGAATATGGGAGATTTAACCACCTTATGATACAGTGAAACACTACTTGGT
ATTGAATACACCACTTGAGGACAATATCATGACTCACGGTTTATCAAGTTTATGTTCTGGAC
TGGTAGCTTCTATTCTGGGAACACCAGCCGATGTCATCAAAAGCAGAATAATGAATCAACCA
CGAGATAAACAAGGAAGGGGACTTTTGTATAAATCATCGACTGACTGCTTGATTGAGGCTGT
TCAAGGTGAAGGATTCATGAGTCTATATAAAGGCTTTTACCATCTTGGCTGAGAATGACCC
CTTGGTCAATGGTGTTCTGGCTTACTTATGAAAAAATCAGAGAGATGAGTGGAGTCAGTCCA
TTTTTAA

FIGURE 236

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77568

><subunit 1 of 1, 323 aa, 1 stop

><MW: 36064, pI: 9.33, NX(S/T): 1

MSVPEEEERLLPLTQRWPRASKFLLSGCAATVAELATFPLDLTKTRLQMGEAALARLGDGA
RESAPYRGMVRTALGIIIEEGFLKLWQGVTPAIYRHVVYSGGRMVITYEHLREVVFVGKSEDEH
YPLWKSVIGGMMAGVIGQFLANPTDLVKVQMMEGKRRKLEGKPLRFRGVHHAFAKILAEGGI
RGLWAGWVPNIQRAALVNMGDLTTYDTVKHYLVLNTPLEDNIMTHGLSSLCSGLVASILGTP
ADVIKSRIMNQPRDKQGRGLLYKSSTDCLIQAVQGEGFMSLYKGFLPSWLRMTPWSMVFWLT
YEKIREMSGVSPF

Transmembrane domains:

amino acids 25-38, 130-147, 233-248

FIGURE 237

CGGACGCGTGGGCGCGGGACGCCGGCAGGGTTGTGGCGCAGCAGTCTCCTTCCTGCGCGCGC
GCCTGAAGTCGGCGTGGGCGTTTGAGGAAGCTGGGATACAGCATTTAATGAAAAATTTATGC
TTAAGAAGTAAAAATGGCAGGCTTCCTAGATAATTTTCGTTGGCCAGAATGTGAATGTATTG
ACTGGAGTGAGAGAAGAAATGCTGTGGCATCTGTTGTCGCAGGTATATTGTTTTTTACAGGC
TGGTGGATAATGATTGATGCAGCTGTGGTGTATCCTAAGCCAGAACAGTTGAACCATGCCTT
TCACACATGTGGTGTATTTTCCACATTGGCTTTCTTCATGATAAATGCTGTATCCAATGCTC
AGGTGAGAGGTGATAGCTATGAAAGCGGCTGTTTAGGAAGAACAGGTGCTCGAGTTTGGCTT
TTCATTGGTTTCATGTTGATGTTTGGGTCACTTATTGCTTCCATGTGGATTCTTTTTTGGTGC
ATATGTTACCCAAAATACTGATGTTTATCCGGGACTAGCTGTGTTTTTTCAAATGCACTTA
TATTTTTTAGCACTCTGATCTACAAATTTGGAAGAACCGAAGAGCTATGGACCTGAGATCAC
TTCTTAAGTCACATTTTCCTTTTGTTATATTCTGTTTGTAGATAGGTTTTTTATCTCTCAGT
ACACATTGCCAAATGGAGTAGATTGTACATTAAATGTTTTGTTTCTTTACATTTTTATGTTT
TGAGTTTTGAAATAGTTTTATGAAATTTCTTTATTTTTTCATTGCATAGACTGTTAATATGTA
TATAATACAAGACTATATGAATTGGATAATGAGTATCAGTTTTTTATTCCTGAGATTTAGAA
CTTGATCTACTCCCTGAGCCAGGGTTACATCATCTTGTCATTTTAGAAGTAACCACTCTTGT
CTCTCTGGCTGGGCACGGTGGCTCATGCCTGTAATCCCAGCACTTTGGGAGGCCGAGGCGGG
CCGATTGCTTGAGGTCAAGTGTTTGAGACCAGCCTGGCCAACATGGCGAAACCCCATCTACT
AAAAATACAAAATTAGCCAGGCATGGTGGTGGGTGCCTGTAATCCCAGCTACCTGGGAGGC
TGAGGCAGGAGAATCGCTTGAACCCGGGGGGCAGAGGTTGCAGTGAGCTGAGTTTGCGCCAC
TGCACTCTAGCCTGGGGGAGAAAAGTGAACTCCCTCTCAAAAAAAGACCACTCTCAGTATC
TCTGATTTCTGAAGATGTACAAAAAATATAGCTTCATATATCTGGAATGAGCACTGAGCCA
TAAAAGGTTTTTCAGCAAGTTGTAACCTATTTTTGGCCTAAAAATGAGGTTTTTTTGGTAAAGA
AAAAATATTTGTTCTTATGTATTGAAGAAGTGACTTTTATATAATGATTTTTTAAATGCCC
AAAGGACTAGTTTGAAAGCTTCTTTTAAAAAGAATTCCTCTAATATGACTTTATGTGAGAA

FIGURE 238

MAGFLDNFRWPECECIDWSERRNAVASVVAGILFFTGWIMIDAADVYPKPEQLNHAFHTCG
VFSTLAFFMINAVSNAQVRGDSYESGCLGRTGARVWLFIGFMLMFGSLIASMWILFGAYVTQ
NTDVYPGLAVFFQNALIFFSTLIYKFG RTEELWT

Important features:

Signal peptide:

amino acids 1-44

Transmembrane domains:

amino acids 23-42 (type II), 60-80, 97-117, 128-148

FIGURE 239

GTTGATGGCAAACCTTCCTCAAAGGAGGGGCAGAGCCTGCGCAGGGCAGGAGCAGCTGGCCCA
CTGGCGGGCCCGCAACACTCCGTCTCACCCCTCTGGGCCCCACTGCATCTAGAGGAGGGCCGTCT
GTGAGGCCACTACCCCTCCAGCAACTGGGAGGTGGGACTGTCAGAAGCTGGCCCAGGGTGGT
GGTCAGCTGGGT CAGGGACCTACGGCACCTGCTGGACCACCTCGCCTTCTCCATCGAAGCAG
GGAAGTGGGAGCCTCGAGCCCTCGGGTGAAGCTGACCCCAAGCCACCCTTCACCTGGACAG
GATGAGAGTGT CAGGTGTGCTTCGCCTCCTGGCCCTCATCTTTGCCATAGTCACGACATGGA
TGTTTATT CGAAGCTACATGAGCTTCAGCATGAAAACCATCCGTCTGCCACGCTGGCTGGCA
GCCTCGCCACCAAGGAGATCCAGGT TAAAAAGTACAAGTGTGGCCTCATCAAGCCCTGCCC
AGCCAACTACTTTGCGTTTAAAATCTGCAGTGGGGCCGCCAACGTCGTGGGCCCTACTATGT
GCTTTGAAGACCGCATGATCATGAGTCCTGTGAAAACAATGTGGGCAGAGGCCTAAACATC
GCCCTGGTGAATGGAACCACGGGAGCTGTGCTGGGACAGAAGGCATTTGACATGTACTCTGG
AGATGTTATGCACCTAGTGAAATTCCTTAAAGAAATTCGGGGGGTGC ACTGGTGCTGGTGG
CCTCCTACGACGATCCAGGGACCAAAATGAACGATGAAAGCAGGAAACTCTTCTGACTTG
GGGAGTTCCTACGCAAAACAACCTGGGCTTCGGGACAGCTGGGTCTTCATAGGAGCCAAAGA
CCTCAGGGGTAAAAGCCCCCTTTGAGCAGTTCTTAAAGAACAGCCCAGACACAAACAAATACG
AGGGATGGCCAGAGCTGCTGGAGATGGAGGGCTGCATGCCCCCGAAGCCATTTTTAGGGTGGC
TGTGGCTCTTCCTCAGCCAGGGGCCTGAAGAAGCTCCTGCCTGACTTAGGAGTCAGAGCCCG
GCAGGGGCTGAGGAGGAGGAGCAGGGGGTGTGCTGCGTGGAAGGTGCTGCAGGTCCTTGACGC
TGTGTCGCGCCTCTCCTCCTCGGAAACAGAACCTCCCACAGCACATCCTACCCGGAAGACC
AGCCTCAGAGGGTCCTTCTGGAACCAGCTGTCTGTGGAGAGAATGGGGTGCTTTCGTCAGGG
ACTGCTGACGGCTGGTCTTGAGGAAGGACAAACTGCCCAGACTTGAGCCCAATTAAATTTTA
TTTTTGCTGGTTTTTGAAAAAAAAAAAAAAAAAAAAA

FIGURE 240

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA59814

<subunit 1 of 1, 224 aa, 1 stop

<MW: 24963, pI: 9.64, NX(S/T): 1

MRVSGVLRLLALIFAIVTTWMFIRSYMSFSMKTIRLPRWLAASPTKEIQVKKYKCGLIKPCP
ANYFAFKICSGAANVVGPTMCFEDRMIMSPVKNNVGRGLNIALVNGTTGAVLGQKAFDMYSG
DVMHLVKFLKEIPGGALVLVASYDDPGTKMNDESRKLFSDLGSSYAKQLGFRDSWVFIGAKD
LRGKSPFEQFLKNSPDTNKYEGWPELLEMEGCMPPKPF

Important features:

Signal peptide:

amino acids 1-15

ATP/GTP-binding site motif A (P-loop).

amino acids 184-191

N-glycosylation site.

amino acids 107-110

FIGURE 241

GAGACTGCAGAGGGAGATAAAGAGAGAGGGCAAAGAGGCAGCAAGAGATTTGTCCTGGGGAT
CCAGAAACCCATGATAACCCTACTGAACACCGAATCCCCTGGAAGCCCACAGAGACAGAGACA
GCAAGAGAAGCAGAGATAAATACACTCACGCCAGGAGCTCGCTCGCTCTCTCTCTCTCTC
TCACTCCTCCCTCCCTCTCTCTCTGCCTGTCCTAGTCCTCTAGTCCTCAAATCCCAGTCCC
CTGCACCCCTTCCTGGGACACTATGTTGTTCTCCGCCCTCCTGCTGGAGGTGATTTGGATCC
TGGCTGCAGATGGGGGTCAACACTGGACGTATGAGGGCCACATGGTCAGGACCATTGGCCA
GCCTCTTACCCTGAGTGTGGAAACAATGCCAGTCGCCCATCGATATTCAGACAGACAGTGT
GACATTTGACCCTGATTTGCCTGCTCTGCAGCCCCACGGATATGACCAGCCTGGCACCGAGC
CTTTGGACCTGCACAACAATGGCCACACAGTGCAACTCTCTCTGCCCTCTACCCTGTATCTG
GGTGGACTTCCCCGAAAATATGTAGCTGCCAGCTCCACCTGCACTGGGGTCAGAAAGGATC
CCCAGGGGGGTCAGAACACCAGATCAACAGTGAAGCCACATTTGCAGAGCTCCAATTGTAC
ATTATGACTCTGATTCCTATGACAGCTTGAGTGAGGCTGCTGAGAGGCCTCAGGGCCTGGCT
GTCCTGGGCATCCTAATTGAGGTGGGTGAGACTAAGAATATAGCTTATGAACACATTCTGAG
TCACTTGCAATGAAGTCAGGCATAAAGATCAGAAGACCTCAGTGCCTCCCTTCAACCTAAGAG
AGCTGCTCCCCAAACAGCTGGGGCAGTACTTCCGCTACAATGGCTCGCTCACAACTCCCCCT
TGCTACCAGAGTGTGCTCTGGACAGTTTTTTATAGAAGGTCCCAGATTTCAATGGAACAGCT
GGAAAAGCTTCAGGGGACATTGTTCTCCACAGAAGAGGAGCCCTCTAAGCTTCTGGTACAGA
ACTACCGAGCCCTTCAGCCTCTCAATCAGCGCATGGTCTTTGCTTCTTTCATCCAAGCAGGA
TCCTCGTATACCACAGGTGAAATGCTGAGTCTAGGTGTAGGAATCTTGGTTGGCTGTCTCTG
CCTTCTCCTGGCTGTTTATTTTATTGCTAGAAAGATTTCGGAAGAAGAGGCTGGAAAACCGAA
AGAGTGTGGTCTTCACCTCAGCACAAGCCACGACTGAGGCATTAAATTCCTTCTCAGATACCA
TGGATGTGGATGACTTCCCTTCATGCCTATCAGGAAGCCTCTAAAATGGGGTGTAGGATCTG
GCCAGAAACACTGTAGGAGTAGTAAGCAGATGTCCTCCTTCCCCTGGACATCTCTTAGAGAG
GAATGGACCCAGGCTGTCATTCCAGGAAGAACTGCAGAGCCTTCAGCCTCTCCAAACATGTA
GGAGGAAATGAGGAAATCGCTGTGTTGTTAATGCAGAGANCAAACTCTGTTTAGTTGCAGGG
GAAGTTTGGGATATAACCCCAAAGTCCTCTACCCCTCACTTTTATGGCCCTTTCCTAGATA
TACTGCGGGATCTCTCCTTAGGATAAAGAGTTGCTGTTGAAGTTGTATATTTTGTATCAATA
TATTTGGAAATTAAAGTTTCTGACTTT

244/270

FIGURE 242

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA62812
><subunit 1 of 1, 337 aa, 1 stop
><MW: 37668, pI: 6.27, NX(S/T): 1
MLFSALLLEVIWILAADGGQHWTYEGPHGQDHPASYPECGNNAQSPIDIQTDSVTFDPDLP
ALQPHGYDQPGTEPLDLHNNGHTVQLSLPSTLYLGGLPRKYVAAQLHLHWGQKGSPGGSEHQ
INSEATFAELHIVHYDSYDSLSEAAERPQGLAVLGILIEVGETKNIAYEHILSHLHEVRH
KDQKTSVPPFNLRELLPKQLGQYFRYNGSLTTPPCYQSVLWTVFYRRSQISMEQLEKLQGT
FSTEEEPSKLLVQNYRALQPLNQRMVFAFIQAGSSYTTGEMLSLGVGILVGCLCLLLAVYF
IARKIRKKRLENRKS VVFTSAQATTEA

Important features of the protein:

Signal peptide:

amino acids 1-15

Transmembrane domain:

amino acids 291-310

N-glycosylation site.

amino acids 213-216

Eukaryotic-type carbonic anhydrases proteins

amino acids 197-245, 104-140, 22-69

FIGURE 243

AATTTTTACCAGAGTAACTTGAGAAACCAACTGGACCTTGAGTATTGTACATTTTGCCTC
GTGGACCCAAAGGTAGCAATCTGAAACATGAGGAGTACGATTCTACTGTTTTGTCTTCTAGG
ATCAACTCGGTCATTACCACAGCTCAAACCTGCTTTGGGACTCCCTCCACAAAACCTGGCTC
CGGATCAGGGAACACTACCAAACCAACAGCAGTCAAATCAGGTCTTTCCTTCTTTAAGTCTG
ATACCATTAACACAGATGCTCACACTGGGGCCAGATCTGCATCTGTTAAATCCTGCTGCAGG
AATGACACCTGGTACCCAGACCCACCCATTGACCCTGGGAGGGTTGAATGTACAACAGCAAC
TGCACCCACATGTGTTACCAATTTTTGTACACAACCTGGAGCCCAGGGCACTATCCTAAGC
TCAGAGGAATTGCCACAAATCTTCACGAGCCTCATCATCCATTCCTTGTTCCCGGGAGGCAT
CCTGCCCACCAGTCAGGCAGGGGCTAATCCAGATGTCCAGGATGGAAGCCTTCCAGCAGGAG
GAGCAGGTGTAAATCCTGCCACCCAGGGAACCCAGCAGGCCGCCTCCCAACTCCAGTGGC
ACAGATGACGACTTTCAGTGACCACCCCTGCAGGCATCCAAAGGAGCACACATGCCATCGA
GGAAGCCACCACAGAATCAGCAAATGGAATTCAGTAAGCTGTTTCAAATTTTTTCAACTAAG
CTGCCTCGAATTTGGTGATACATGTGAATCTTTATCATTTGATTATATTATGGAATAGATTGA
GACACATTGGATAGTCTTAGAAGAAATTAATTCCTTAATTTACCTGAAAATATTCTTGAAATT
TCAGAAAATATGTTCTATGTAGAGAATCCCAACTTTTAAAAACAATAATTCAATGGATAAAT
CTGTCTTTGAAATATAACATTATGCTGCCTGGATGATATGCATATTA AACATATTTGGAAA
ACTGGAA
AAAAAAAAAAAAAAAAAAAAA

FIGURE 244

MRSTILLFCLLGSTRSLPQLKPALGLPPTKLAPDQGTLPNQQQSNQVFPSLSLIPLTQM
LTLGPDHLHLLNPAAGMTPGTQTHPLTLGGLNVQQQLHPHVLPIFVTQLGAQGTLISSEE
LPQIFTSLIIHSLFPGGILPTSQAGANPDVQDGSLPAGGAGVNPATQGTPAGRLPTPSG
TDDDFAVTTPAGIQRSTHAIEEATTESANGIQ

Signal peptide:

amino acids 1-16

FIGURE 245

GGAGAGAGGCGCGCGGGTGAAAGGCGCATTGATGCAGCCTGCGGCGGCCTCGGAGCGCGGCG
GAGCCAGACGCTGACCACGTTCCCTCTCCTCGGTCTCCTCCGCCTCCAGCTCCGCGCTGCCCC
GCAGCCGGGAGCCATGCGACCCAGGGCCCCGCGCCTCCCCGCAGCGGCTCCGCGGCCTCC
TGCTGCTCCTGCTGCTGCAGCTGCCCCGCGCCGTGAGCGCCTCTGAGATCCCCAAGGGGAAG
CAAAAGGCGCAGCTCCGGCAGAGGGAGGTGGTGGACCTGTATAATGGAATGTGCTTACAAGG
GCCAGCAGGAGTGCCTGGTCGAGACGGGAGCCCTGGGGCCAATGTTATTCCGGGTACACCTG
GGATCCCAGGTGCGGATGGATTCAAAGGAGAAAAGGGGGAATGTCTGAGGGAAAGCTTTGAG
GAGTCCTGGACACCCAACTACAAGCAGTGTTTCATGGAGTTCATTGAATTATGGCATAGATCT
TGGGAAAATTGCGGAGTGACATTTACAAAGATGCGTTCAAATAGTGCTCTAAGAGTTTTGT
TCAGTGGCTCACTTCGGCTAAAATGCAGAAATGCATGCTGTGAGCGTTGGTATTTACATTC
AATGGAGCTGAATGTTTCAGGACCTCTTCCCATTTGAAGCTATAATTTATTTGGACCAAGGAAG
CCCTGAAATGAATTCAACAATTAATATTCATCGCACTTCTTCTGTGGAAGGACTTTGTGAAG
GAATTGGTGCTGGATTAGTGGATGTTGCTATCTGGGTTGGCACTTGTTTCAGATTACCCAAAA
GGAGATGCTTCTACTGGATGGAATTCAGTTTCTCGCATCATTATTGAAGAACTACCAAAATA
AATGCTTTAATTTTCATTTGCTACCTCTTTTTTTATTATGCCTTGGAATGGTTCACTTAAAT
GACATTTTAAATAAGTTTATGTATACATCTGAATGAAAAGCAAAGCTAAATATGTTTACAGA
CCAAAGTGTGATTTACACTGTTTTTAAATCTAGCATTATTCATTTTGCTTCAATCAAAAGT
GGTTTCAATATTTTTTTTAGTTGGTTAGAATACTTTCTTCATAGTCACATTCTCTCAACCTA
TAATTTGGAATATTGTTGTGGTCTTTTGTTTTTTCTCTTAGTATAGCATTTTTTAAAAAATA
TAAAAGCTACCAATCTTTGTACAATTTGTAAATGTTAAGAATTTTTTTTATATCTGTAAAT
AAAAATTATTTCCAACA

FIGURE 246

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76393

><subunit 1 of 1, 243 aa, 1 stop

><MW: 26266, pI: 8.43, NX(S/T): 1

MRPQGPAASPQRLRGLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPA
PGRDGSPGANVIPGTPGIPGRDGFKEKGECLRESFEESWTPNYKQCSWSSLNYGIDLGKIA
ECTFTKMRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEAIYLDQGSP
STINIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIIIEELPK

Signal peptide:

amino acids 1-30

Transmembrane domain:

amino acids 195-217

FIGURE 247A

PRO	XXXXXXXXXXXXXXXXXX	(Length = 15 amino acids)
Comparison Protein	XXXXXXYYYYYYY	(Length = 12 amino acids)

% amino acid sequence identity =

(the number of identically matching amino acid residues between the two polypeptide sequences as determined by ALIGN-2) divided by (the total number of amino acid residues of the PRO polypeptide) =

5 divided by 15 = 33.3%

FIGURE 247B

PRO	XXXXXXXXXX	(Length = 10 amino acids)
Comparison Protein	XXXXXYYYYYZZYZ	(Length = 15 amino acids)

% amino acid sequence identity =

(the number of identically matching amino acid residues between the two polypeptide sequences as determined by ALIGN-2) divided by (the total number of amino acid residues of the PRO polypeptide) =

5 divided by 10 = 50%

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FIGURE 247C

PRO-DNA	NNNNNNNNNNNNNNNN	(Length = 14 nucleotides)
Comparison DNA	NNNNNNLLLLLLLLLLL	(Length = 16 nucleotides)

% nucleic acid sequence identity =

(the number of identically matching nucleotides between the two nucleic acid sequences as determined by ALIGN-2) divided by (the total number of nucleotides of the PRO-DNA nucleic acid sequence) =

6 divided by 14 = 42.9%

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FIGURE 247D

PRO-DNA	NNNNNNNNNNNNNN	(Length = 12 nucleotides)
Comparison DNA	NNNNLLLTVV	(Length = 9 nucleotides)

% nucleic acid sequence identity =

(the number of identically matching nucleotides between the two nucleic acid sequences as determined by ALIGN-2) divided by (the total number of nucleotides of the PRO-DNA nucleic acid sequence) =

4 divided by 12 = 33.3%

FIGURE 248A

```

/*
 *
 * C-C increased from 12 to 15
 * Z is average of EQ
 * B is average of ND
 * match with stop is _M: stop-stop = 0; J (joker) match = 0
 */
#define _M      -8      /* value of a match with a stop */

int      _day[26][26] = {
/*      A B C D E F G H I J K L M N O P Q R S T U V W X Y Z */
/* A */      { 2, 0, -2, 0, 0, -4, 1, -1, -1, 0, -1, -2, -1, 0, _M, 1, 0, -2, 1, 1, 0, 0, -6, 0, -3, 0 },
/* B */      { 0, 3, -4, 3, 2, -5, 0, 1, -2, 0, 0, -3, -2, 2, _M, -1, 1, 0, 0, 0, 0, -2, -5, 0, -3, 1 },
/* C */      { -2, -4, 15, -5, -5, -4, -3, -3, -2, 0, -5, -6, -5, -4, _M, -3, -5, -4, 0, -2, 0, -2, -8, 0, 0, -5 },
/* D */      { 0, 3, -5, 4, 3, -6, 1, 1, -2, 0, 0, -4, -3, 2, _M, -1, 2, -1, 0, 0, 0, -2, -7, 0, -4, 2 },
/* E */      { 0, 2, -5, 3, 4, -5, 0, 1, -2, 0, 0, -3, -2, 1, _M, -1, 2, -1, 0, 0, 0, -2, -7, 0, -4, 3 },
/* F */      { -4, -5, -4, -6, -5, 9, -5, -2, 1, 0, -5, 2, 0, -4, _M, -5, -5, -4, -3, -3, 0, -1, 0, 0, 7, -5 },
/* G */      { 1, 0, -3, 1, 0, -5, 5, -2, -3, 0, -2, -4, -3, 0, _M, -1, -1, -3, 1, 0, 0, -1, -7, 0, -5, 0 },
/* H */      { -1, 1, -3, 1, 1, -2, -2, 6, -2, 0, 0, -2, -2, 2, _M, 0, 3, 2, -1, -1, 0, -2, -3, 0, 0, 2 },
/* I */      { -1, -2, -2, -2, -2, 1, -3, -2, 5, 0, -2, 2, 2, -2, _M, -2, -2, -2, -1, 0, 0, 4, -5, 0, -1, -2 },
/* J */      { 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, _M, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0 },
/* K */      { -1, 0, -5, 0, 0, -5, -2, 0, -2, 0, 5, -3, 0, 1, _M, -1, 1, 3, 0, 0, 0, -2, -3, 0, -4, 0 },
/* L */      { -2, -3, -6, -4, -3, 2, -4, -2, 2, 0, -3, 6, 4, -3, _M, -3, -2, -3, -3, -1, 0, 2, -2, 0, -1, -2 },
/* M */      { -1, -2, -5, -3, -2, 0, -3, -2, 2, 0, 0, 4, 6, -2, _M, -2, -1, 0, -2, -1, 0, 2, -4, 0, -2, -1 },
/* N */      { 0, 2, -4, 2, 1, -4, 0, 2, -2, 0, 1, -3, -2, 2, _M, -1, 1, 0, 1, 0, 0, -2, -4, 0, -2, 1 },
/* O */      { _M, _M, _M, _M, _M, _M, _M, _M, _M, _M, _M, _M, _M, _M, _M, _M, _M, _M, _M, _M, _M, _M, _M, _M, _M },
/* P */      { 1, -1, -3, -1, -1, -5, -1, 0, -2, 0, -1, -3, -2, -1, _M, 6, 0, 0, 1, 0, 0, -1, -6, 0, -5, 0 },
/* Q */      { 0, 1, -5, 2, 2, -5, -1, 3, -2, 0, 1, -2, -1, 1, _M, 0, 4, 1, -1, -1, 0, -2, -5, 0, -4, 3 },
/* R */      { -2, 0, -4, -1, -1, -4, -3, 2, -2, 0, 3, -3, 0, 0, _M, 0, 1, 6, 0, -1, 0, -2, 2, 0, -4, 0 },
/* S */      { 1, 0, 0, 0, 0, -3, 1, -1, -1, 0, 0, -3, -2, 1, _M, 1, -1, 0, 2, 1, 0, -1, -2, 0, -3, 0 },
/* T */      { 1, 0, -2, 0, 0, -3, 0, -1, 0, 0, 0, -1, -1, 0, _M, 0, -1, -1, 1, 3, 0, 0, -5, 0, -3, 0 },
/* U */      { 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, _M, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0 },
/* V */      { 0, -2, -2, -2, -2, -1, -1, -2, 4, 0, -2, 2, 2, -2, _M, -1, -2, -2, -1, 0, 0, 4, -6, 0, -2, -2 },
/* W */      { -6, -5, -8, -7, -7, 0, -7, -3, -5, 0, -3, -2, -4, -4, _M, -6, -5, 2, -2, -5, 0, -6, 17, 0, 0, -6 },
/* X */      { 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, _M, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0 },
/* Y */      { -3, -3, 0, -4, -4, 7, -5, 0, -1, 0, -4, -1, -2, -2, _M, -5, -4, -4, -3, -3, 0, -2, 0, 0, 10, -4 },
/* Z */      { 0, 1, -5, 2, 3, -5, 0, 2, -2, 0, 0, -2, -1, 1, _M, 0, 3, 0, 0, 0, 0, -2, -6, 0, -4, 4 }
};

```

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FIGURE 248B

```

/*
*/
#include <stdio.h>
#include <ctype.h>

#define MAXJMP      16      /* max jumps in a diag */
#define MAXGAP      24      /* don't continue to penalize gaps larger than this */
#define JMPS        1024    /* max jmps in an path */
#define MX          4       /* save if there's at least MX-1 bases since last jmp */

#define DMAT        3       /* value of matching bases */
#define DMIS        0       /* penalty for mismatched bases */
#define DINS0       8       /* penalty for a gap */
#define DINS1       1       /* penalty per base */
#define PINS0       8       /* penalty for a gap */
#define PINS1       4       /* penalty per residue */

struct jmp {
    short          n[MAXJMP];      /* size of jmp (neg for dely) */
    unsigned short x[MAXJMP];      /* base no. of jmp in seq x */
};
/* limits seq to 2^16 - 1 */

struct diag {
    int            score;          /* score at last jmp */
    long           offset;         /* offset of prev block */
    short          ijmp;           /* current jmp index */
    struct jmp     jp;             /* list of jmps */
};

struct path {
    int            spc;            /* number of leading spaces */
    short          n[JMPS];        /* size of jmp (gap) */
    int            x[JMPS];        /* loc of jmp (last elem before gap) */
};

char              *ofile;         /* output file name */
char              *namex[2];      /* seq names: getseqs() */
char              *prog;          /* prog name for err msgs */
char              *seqx[2];       /* seqs: getseqs() */
int               dmax;           /* best diag: nw() */
int               dmax0;          /* final diag */
int               dna;            /* set if dna: main() */
int               endgaps;        /* set if penalizing end gaps */
int               gapx, gapy;      /* total gaps in seqs */
int               len0, len1;     /* seq lens */
int               ngapx, ngapy;    /* total size of gaps */
int               smax;           /* max score: nw() */
int               *xbm;           /* bitmap for matching */
long              offset;         /* current offset in jmp file */
struct            diag            /* holds diagonals */
struct            path            /* holds path for seqs */
{
    *dx;
    pp[2];
};

char              *calloc(), *malloc(), *index(), *strcpy();
char              *getseq(), *g_calloc();

```

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FIGURE 248C

```

/* Needleman-Wunsch alignment program
*
* usage: prog file1 file2
*   where file1 and file2 are two dna or two protein sequences.
*   The sequences can be in upper- or lower-case and may contain ambiguity
*   Any lines beginning with ';', '>' or '<' are ignored
*   Max file length is 65535 (limited by unsigned short x in the jmp struct)
*   A sequence with 1/3 or more of its elements ACGTU is assumed to be DNA
*   Output is in the file "align.out"
*
* The program may create a tmp file in /tmp to hold info about traceback.
* Original version developed under BSD 4.3 on a vax 8650
*/
#include "nw.h"
#include "day.h"

static  _dbval[26] = {
    1,14,2,13,0,0,4,11,0,0,12,0,3,15,0,0,0,5,6,8,8,7,9,0,10,0
};

static  _pbval[26] = {
    1, 2|(1<<('D'-'A'))|(1<<('N'-'A')), 4, 8, 16, 32, 64,
    128, 256, 0xFFFFFFFF, 1<<10, 1<<11, 1<<12, 1<<13, 1<<14,
    1<<15, 1<<16, 1<<17, 1<<18, 1<<19, 1<<20, 1<<21, 1<<22,
    1<<23, 1<<24, 1<<25|(1<<('E'-'A'))|(1<<('Q'-'A'))
};

main(ac, av)                                main
{
    int    ac;
    char   *av[];

    prog = av[0];
    if (ac != 3) {
        fprintf(stderr, "usage: %s file1 file2\n", prog);
        fprintf(stderr, "where file1 and file2 are two dna or two protein sequences.\n");
        fprintf(stderr, "The sequences can be in upper- or lower-case\n");
        fprintf(stderr, "Any lines beginning with ';' or '<' are ignored\n");
        fprintf(stderr, "Output is in the file \"align.out\"\n");
        exit(1);
    }
    namex[0] = av[1];
    namex[1] = av[2];
    seqx[0] = getseq(namex[0], &len0);
    seqx[1] = getseq(namex[1], &len1);
    xbm = (dna)? _dbval : _pbval;

    endgaps = 0;                                /* 1 to penalize endgaps */
    ofile = "align.out";                        /* output file */

    nw();                                       /* fill in the matrix, get the possible jmps */
    readjmps();                               /* get the actual jmps */
    print();                                  /* print stats, alignment */

    cleanup(0);                               /* unlink any tmp files */
}

```

FIGURE 248D

```

/* do the alignment, return best score: main()
 * dna: values in Fitch and Smith, PNAS, 80, 1382-1386, 1983
 * pro: PAM 250 values
 * When scores are equal, we prefer mismatches to any gap, prefer
 * a new gap to extending an ongoing gap, and prefer a gap in seqx
 * to a gap in seq y.
 */
nw()
{
    char          *px, *py;          /* seqs and ptrs */
    int           *ndely, *dely;      /* keep track of dely */
    int           ndelx, delx;        /* keep track of delx */
    int           *tmp;               /* for swapping row0, row1 */
    int           mis;                /* score for each type */
    int           ins0, ins1;         /* insertion penalties */
    register      id;                 /* diagonal index */
    register      ij;                 /* jmp index */
    register      *col0, *col1;       /* score for curr, last row */
    register      xx, yy;             /* index into seqs */

    dx = (struct diag *)g_calloc("to get diags", len0+len1+1, sizeof(struct diag));

    ndely = (int *)g_calloc("to get ndely", len1+1, sizeof(int));
    dely = (int *)g_calloc("to get dely", len1+1, sizeof(int));
    col0 = (int *)g_calloc("to get col0", len1+1, sizeof(int));
    col1 = (int *)g_calloc("to get col1", len1+1, sizeof(int));
    ins0 = (dna)? DINS0 : PINS0;
    ins1 = (dna)? DINS1 : PINS1;

    smax = -10000;
    if (endgaps) {
        for (col0[0] = dely[0] = -ins0, yy = 1; yy <= len1; yy++) {
            col0[yy] = dely[yy] = col0[yy-1] - ins1;
            ndely[yy] = yy;
        }
        col0[0] = 0;          /* Waterman Bull Math Biol 84 */
    }
    else
        for (yy = 1; yy <= len1; yy++)
            dely[yy] = -ins0;

    /* fill in match matrix
     */
    for (px = seqx[0], xx = 1; xx <= len0; px++, xx++) {
        /* initialize first entry in col
         */
        if (endgaps) {
            if (xx == 1)
                col1[0] = delx = -(ins0+ins1);
            else
                col1[0] = delx = col0[0] - ins1;
            ndelx = xx;
        }
        else {
            col1[0] = 0;
            delx = -ins0;
            ndelx = 0;
        }
    }
}

```

nw

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FIGURE 248E

...nw

```

for (py = seqx[1], yy = 1; yy <= len1; py++, yy++) {
    mis = col0[yy-1];
    if (dna)
        mis += (xbm[*px-'A']&xbm[*py-'A'])? DMAT : DMIS;
    else
        mis += _day[*px-'A'][*py-'A'];

    /* update penalty for del in x seq;
     * favor new del over ongong del
     * ignore MAXGAP if weighting endgaps
     */
    if (endgaps || ndely[yy] < MAXGAP) {
        if (col0[yy] - ins0 >= dely[yy]) {
            dely[yy] = col0[yy] - (ins0 + ins1);
            ndely[yy] = 1;
        } else {
            dely[yy] -= ins1;
            ndely[yy]++;
        }
    } else {
        if (col0[yy] - (ins0 + ins1) >= dely[yy]) {
            dely[yy] = col0[yy] - (ins0 + ins1);
            ndely[yy] = 1;
        } else
            ndely[yy]++;
    }

    /* update penalty for del in y seq;
     * favor new del over ongong del
     */
    if (endgaps || ndelx < MAXGAP) {
        if (col1[yy-1] - ins0 >= delx) {
            delx = col1[yy-1] - (ins0 + ins1);
            ndelx = 1;
        } else {
            delx -= ins1;
            ndelx++;
        }
    } else {
        if (col1[yy-1] - (ins0 + ins1) >= delx) {
            delx = col1[yy-1] - (ins0 + ins1);
            ndelx = 1;
        } else
            ndelx++;
    }

    /* pick the maximum score; we're favoring
     * mis over any del and delx over dely
     */
}

```

FIGURE 248F

...nw

```

id = xx - yy + len1 - 1;
if (mis >= delx && mis >= dely[yy])
    coll[yy] = mis;
else if (delx >= dely[yy]) {
    coll[yy] = delx;
    ij = dx[id].ijmp;
    if (dx[id].jp.n[0] && (!dna || (ndelx >= MAXJMP
    && xx > dx[id].jp.x[ij] + MX) || mis > dx[id].score + DINS0)) {
        dx[id].ijmp++;
        if (++ij >= MAXJMP) {
            writejumps(id);
            ij = dx[id].ijmp = 0;
            dx[id].offset = offset;
            offset += sizeof(struct jmp) + sizeof(offset);
        }
        dx[id].jp.n[ij] = ndelx;
        dx[id].jp.x[ij] = xx;
        dx[id].score = delx;
    }
    else {
        coll[yy] = dely[yy];
        ij = dx[id].ijmp;

        if (dx[id].jp.n[0] && (!dna || (ndely[yy] >= MAXJMP
        && xx > dx[id].jp.x[ij] + MX) || mis > dx[id].score + DINS0)) {
            dx[id].ijmp++;
            if (++ij >= MAXJMP) {
                writejumps(id);
                ij = dx[id].ijmp = 0;
                dx[id].offset = offset;
                offset += sizeof(struct jmp) + sizeof(offset);
            }
            dx[id].jp.n[ij] = -ndely[yy];
            dx[id].jp.x[ij] = xx;
            dx[id].score = dely[yy];
        }
        if (xx == len0 && yy < len1) {
            /* last col
            */
            if (endgaps)
                coll[yy] -= ins0 + ins1 * (len1 - yy);
            if (coll[yy] > smax) {
                smax = coll[yy];
                dmax = id;
            }
        }
    }
    if (endgaps && xx < len0)
        coll[yy-1] -= ins0 + ins1 * (len0 - xx);
    if (coll[yy-1] > smax) {
        smax = coll[yy-1];
        dmax = id;
    }
    tmp = col0; col0 = coll; coll = tmp;
}
(void) free((char *)ndely);
(void) free((char *)dely);
(void) free((char *)col0);
(void) free((char *)coll);
}

```

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FIGURE 248G

```

/*
 *
 * print() -- only routine visible outside this module
 *
 * static:
 * getmat() -- trace back best path, count matches: print()
 * pr_align() -- print alignment of described in array p[]: print()
 * dumpblock() -- dump a block of lines with numbers. stars: pr_align()
 * nums() -- put out a number line: dumpblock()
 * putline() -- put out a line (name, [num], seq, [num]): dumpblock()
 * stars() -- put a line of stars: dumpblock()
 * stripname() -- strip any path and prefix from a seqname
 */

#include "nw.h"

#define SPC      3
#define P_LINE  256 /* maximum output line */
#define P_SPC    3   /* space between name or num and seq */

extern _day[26][26];
int olen; /* set output line length */
FILE *fx; /* output file */

print()
{
    int lx, ly, firstgap, lastgap; /* overlap */

    if ((fx = fopen(ofile, "w")) == 0) {
        fprintf(stderr, "%s: can't write %s\n", prog, ofile);
        cleanup(1);
    }
    fprintf(fx, "<first sequence: %s (length = %d)\n", namex[0], len0);
    fprintf(fx, "<second sequence: %s (length = %d)\n", namex[1], len1);
    olen = 60;
    lx = len0;
    ly = len1;
    firstgap = lastgap = 0;
    if (dmax < len1 - 1) { /* leading gap in x */
        pp[0].spc = firstgap = len1 - dmax - 1;
        ly -= pp[0].spc;
    }
    else if (dmax > len1 - 1) { /* leading gap in y */
        pp[1].spc = firstgap = dmax - (len1 - 1);
        lx -= pp[1].spc;
    }
    if (dmax0 < len0 - 1) { /* trailing gap in x */
        lastgap = len0 - dmax0 - 1;
        lx -= lastgap;
    }
    else if (dmax0 > len0 - 1) { /* trailing gap in y */
        lastgap = dmax0 - (len0 - 1);
        ly -= lastgap;
    }
    getmat(lx, ly, firstgap, lastgap);
    pr_align();
}

```

print

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FIGURE 248H

```

/*
 * trace back the best path, count matches
 */
static
getmat(lx, ly, firstgap, lastgap)
    int      lx, ly;          /* "core" (minus endgaps) */
    int      firstgap, lastgap; /* leading trailing overlap */
{
    int      nm, i0, i1, siz0, siz1;
    char      outx[32];
    double    pct;
    register  n0, n1;
    register char *p0, *p1;

    /* get total matches, score
    */
    i0 = i1 = siz0 = siz1 = 0;
    p0 = seqx[0] + pp[1].spc;
    p1 = seqx[1] + pp[0].spc;
    n0 = pp[1].spc + 1;
    n1 = pp[0].spc + 1;

    nm = 0;
    while ( *p0 && *p1 ) {
        if (siz0) {
            p1++;
            n1++;
            siz0--;
        }
        else if (siz1) {
            p0++;
            n0++;
            siz1--;
        }
        else {
            if (xbm[*p0-'A']&xbm[*p1-'A'])
                nm++;
            if (n0++ == pp[0].x[i0])
                siz0 = pp[0].n[i0++];
            if (n1++ == pp[1].x[i1])
                siz1 = pp[1].n[i1++];
            p0++;
            p1++;
        }
    }

    /* pct homology:
    * if penalizing endgaps, base is the shorter seq
    * else, knock off overhangs and take shorter core
    */
    if (endgaps)
        lx = (len0 < len1)? len0 : len1;
    else
        lx = (lx < ly)? lx : ly;
    pct = 100.*((double)nm)/((double)lx);
    fprintf(fx, "\n");
    fprintf(fx, "< %d match%s in an overlap of %d: %.2f percent similarity\n",
        nm, (nm == 1)? "" : "es", lx, pct);
}

```

getmat

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FIGURE 248I

```

fprintf(fx, "< gaps in first sequence: %d", gapx);
if (gapx) {
    (void) sprintf(outx, " (%d %s%s)",
        gapx, (dna)? "base":"residue", (gapx == 1)? "" : "s");
    fprintf(fx, "%s", outx);

    fprintf(fx, ", gaps in second sequence: %d", gapy);
    if (gapy) {
        (void) sprintf(outx, " (%d %s%s)",
            gapy, (dna)? "base":"residue", (gapy == 1)? "" : "s");
        fprintf(fx, "%s", outx);
    }
    if (dna)
        fprintf(fx,
            "\n< score: %d (match = %d, mismatch = %d, gap penalty = %d + %d per base)\n",
            smax, DMAT, DMIS, DINS0, DINS1);
    else
        fprintf(fx,
            "\n< score: %d (Dayhoff PAM 250 matrix, gap penalty = %d + %d per residue)\n",
            smax, PINS0, PINS1);
    if (endgaps)
        fprintf(fx,
            "< endgaps penalized. left endgap: %d %s%s, right endgap: %d %s%s\n",
            firstgap, (dna)? "base" : "residue", (firstgap == 1)? "" : "s",
            lastgap, (dna)? "base" : "residue", (lastgap == 1)? "" : "s");
    else
        fprintf(fx, "< endgaps not penalized\n");
}

static      nm;          /* matches in core -- for checking */
static      lmax;        /* lengths of stripped file names */
static      ij[2];       /* jmp index for a path */
static      nc[2];       /* number at start of current line */
static      ni[2];       /* current elem number -- for gapping */
static      siz[2];
static char *ps[2];      /* ptr to current element */
static char *po[2];      /* ptr to next output char slot */
static char out[2][P_LINE]; /* output line */
static char star[P_LINE]; /* set by stars() */

/*
 * print alignment of described in struct path pp[]
 */
static
pr_align()
{
    int      nn;          /* char count */
    int      more;
    register i;

    for (i = 0, lmax = 0; i < 2; i++) {
        nn = stripname(name[i]);
        if (nn > lmax)
            lmax = nn;

        nc[i] = 1;
        ni[i] = 1;
        siz[i] = ij[i] = 0;
        ps[i] = seqx[i];
        po[i] = out[i];
    }
}

```

...getmat

pr_align

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FIGURE 248J

```

for (nn = nm = 0, more = 1; more;) {
    for (i = more = 0; i < 2; i++) {
        /*
         * do we have more of this sequence?
         */
        if (!*ps[i])
            continue;

        more++;

        if (pp[i].spc) { /* leading space */
            *po[i]++ = ' ';
            pp[i].spc--;
        }
        else if (siz[i]) { /* in a gap */
            *po[i]++ = '-';
            siz[i]--;
        }
        else {
            /* we're putting a seq element
             */
            *po[i] = *ps[i];
            if (islower(*ps[i]))
                *ps[i] = toupper(*ps[i]);
            po[i]++;
            ps[i]++;

            /*
             * are we at next gap for this seq?
             */
            if (ni[i] == pp[i].x[ij[i]]) {
                /*
                 * we need to merge all gaps
                 * at this location
                 */
                siz[i] = pp[i].n[ij[i] + +];
                while (ni[i] == pp[i].x[ij[i]])
                    siz[i] += pp[i].n[ij[i] + +];
            }
            ni[i]++;
        }
    }
    if (++nn == olen || !more && nn) {
        dumpblock();
        for (i = 0; i < 2; i++)
            po[i] = out[i];
        nn = 0;
    }
}

/*
 * dump a block of lines, including numbers, stars: pr_align()
 */
static
dumpblock()
{
    register i;

    for (i = 0; i < 2; i++)
        *po[i]-- = '\0';
}

```

...pr_align

dumpbl ck

FIGURE 248K

...dumpblock

```

(void) putc('\n', fx);
for (i = 0; i < 2; i++) {
    if (*out[i] && (*out[i] != ' ' || *(po[i]) != ' ')) {
        if (i == 0)
            nums(i);
        if (i == 0 && *out[1])
            stars();
        putline(i);
        if (i == 0 && *out[1])
            fprintf(fx, star);
        if (i == 1)
            nums(i);
    }
}
}

```

```

/*
 * put out a number line: dumpblock()
 */
static
nums(ix)
int ix; /* index in out[] holding seq line */
{
    char nline[P_LINE];
    register i, j;
    register char *pn, *px, *py;

    for (pn = nline, i = 0; i < lmax + P_SPC; i++, pn++)
        *pn = ' ';
    for (i = nc[ix], py = out[ix]; *py; py++, pn++) {
        if (*py == ' ' || *py == '-')
            *pn = ' ';
        else {
            if (i % 10 == 0 || (i == 1 && nc[ix] != 1)) {
                j = (i < 0)? -i : i;
                for (px = pn; j /= 10, px--)
                    *px = j % 10 + '0';
                if (i < 0)
                    *px = '-';
            }
            else
                *pn = ' ';
            i++;
        }
    }
    *pn = '\0';
    nc[ix] = i;
    for (pn = nline; *pn; pn++)
        (void) putc(*pn, fx);
    (void) putc('\n', fx);
}

```

nums

```

/*
 * put out a line (name, [num], seq, [num]): dumpblock()
 */
static
putline(ix)
int ix;
{

```

putline

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FIGURE 248L

...putline

```

int          i;
register char *px;

for (px = namex[ix], i = 0; *px && *px != ':'; px++, i++)
    (void) putc(*px, fx);
for (; i < lmax+P_SPC; i++)
    (void) putc(' ', fx);

/* these count from 1:
 * ni[] is current element (from 1)
 * nc[] is number at start of current line
 */
for (px = out[ix]; *px; px++)
    (void) putc(*px&0x7F, fx);
(void) putc('\n', fx);
}

/*
 * put a line of stars (seqs always in out[0], out[1]): dumpblock()
 */
static
stars()
{
    int          i;
    register char *p0, *p1, cx, *px;

    if (!*out[0] || (*out[0] == ' ' && *(po[0]) == ' ') ||
        !*out[1] || (*out[1] == ' ' && *(po[1]) == ' '))
        return;
    px = star;
    for (i = lmax+P_SPC; i; i--)
        *px++ = ' ';

    for (p0 = out[0], p1 = out[1]; *p0 && *p1; p0++, p1++) {
        if (isalpha(*p0) && isalpha(*p1)) {
            if (xbm[*p0-'A']&xbm[*p1-'A']) {
                cx = '*';
                nm++;
            }
            else if (!dna && _day[*p0-'A'][*p1-'A'] > 0)
                cx = '.';
            else
                cx = ' ';
        }
        else
            cx = ' ';
        *px++ = cx;
    }
    *px++ = '\n';
    *px = '\0';
}

```

stars

FIGURE 248M

```
/*
 * strip path or prefix from pn, return len: pr_align()
 */
static
stripname(pn)
{
    char    *pn;    /* file name (may be path) */

    register char    *px, *py;

    py = 0;
    for (px = pn; *px; px++)
        if (*px == '/')
            py = px + 1;

    if (py)
        (void) strcpy(pn, py);
    return(strlen(pn));
}
```

stripname

FIGURE 248N

```

/*
 * cleanup() -- cleanup any tmp file
 * getseq() -- read in seq, set dna, len, maxlen
 * g_calloc() -- calloc() with error checkin
 * readjumps() -- get the good jumps, from tmp file if necessary
 * writejumps() -- write a filled array of jumps to a tmp file: nw()
 */
#include "nw.h"
#include <sys/file.h>

char    *jname = "/tmp/homgXXXXXX";      /* tmp file for jumps */
FILE    *fj;

int      cleanup();                      /* cleanup tmp file */
long     lseek();

/*
 * remove any tmp file if we blow
 */
cleanup(i)
    int    i;
{
    if (fj)
        (void) unlink(jname);
    exit(i);
}

/*
 * read, return ptr to seq, set dna, len, maxlen
 * skip lines starting with ';', '<', or '>'
 * seq in upper or lower case
 */
char      *
getseq(file, len)
    char    *file;      /* file name */
    int     *len;       /* seq len */
{
    char      line[1024], *pseq;
    register char *px, *py;
    int       natgc, tlen;
    FILE      *fp;

    if ((fp = fopen(file, "r")) == 0) {
        fprintf(stderr, "%s: can't read %s\n", prog, file);
        exit(1);
    }
    tlen = natgc = 0;
    while (fgets(line, 1024, fp)) {
        if (*line == ';' || *line == '<' || *line == '>')
            continue;
        for (px = line; *px != '\n'; px++)
            if (isupper(*px) || islower(*px))
                tlen++;
    }
    if ((pseq = malloc((unsigned)(tlen+6))) == 0) {
        fprintf(stderr, "%s: malloc() failed to get %d bytes for %s\n", prog, tlen+6, file);
        exit(1);
    }
    pseq[0] = pseq[1] = pseq[2] = pseq[3] = '\0';

```

cleanup

getseq

FIGURE 2480

...getseq

```

py = pseq + 4;
*len = tlen;
rewind(fp);

while (fgets(line, 1024, fp)) {
    if (*line == ';' || *line == '<' || *line == '>')
        continue;
    for (px = line; *px != '\n'; px++) {
        if (isupper(*px))
            *py++ = *px;
        else if (islower(*px))
            *py++ = toupper(*px);
        if (index("ATGCU", *(py-1)))
            natgc++;
    }
    *py++ = '\0';
    *py = '\0';
    (void) fclose(fp);
    dna = natgc > (tlen/3);
    return(pseq+4);
}

```

```

char *
g_calloc(msg, nx, sz)

```

g_calloc

```

    char *msg;          /* program, calling routine */
    int nx, sz;          /* number and size of elements */
{
    char *px, *calloc();

    if ((px = calloc((unsigned)nx, (unsigned)sz)) == 0) {
        if (*msg) {
            fprintf(stderr, "%s: g_calloc() failed %s (n=%d, sz=%d)\n", prog, msg, nx, sz);
            exit(1);
        }
    }
    return(px);
}

```

```

/*
 * get final jmps from dx[] or tmp file, set pp[], reset dmax: main()
 */

```

```

readjmps()

```

readjmps

```

{
    int fd = -1;
    int siz, i0, i1;
    register i, j, xx;

    if (fj) {
        (void) fclose(fj);
        if ((fd = open(jname, O_RDONLY, 0)) < 0) {
            fprintf(stderr, "%s: can't open() %s\n", prog, jname);
            cleanup(1);
        }
    }
    for (i = i0 = i1 = 0, dmax0 = dmax, xx = len0; i++) {
        while (1) {
            for (j = dx[dmax].ijmp; j >= 0 && dx[dmax].jp.x[j] >= xx; j--)
                ;

```

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FIGURE 248P

...readjumps

```

    if (j < 0 && dx[dmax].offset && fj) {
        (void) lseek(fd, dx[dmax].offset, 0);
        (void) read(fd, (char *)&dx[dmax].jp, sizeof(struct jmp));
        (void) read(fd, (char *)&dx[dmax].offset, sizeof(dx[dmax].offset));
        dx[dmax].ijmp = MAXJMP-1;
    }
    else
        break;
}
if (i >= JMPS) {
    fprintf(stderr, "%s: too many gaps in alignment\n", prog);
    cleanup(1);
}
if (j >= 0) {
    siz = dx[dmax].jp.n[j];
    xx = dx[dmax].jp.x[j];
    dmax += siz;
    if (siz < 0) {
        /* gap in second seq */
        pp[1].n[i1] = -siz;
        xx += siz;

        /* id = xx - yy + len1 - 1
        */
        pp[1].x[i1] = xx - dmax + len1 - 1;
        gapy++;
        ngapy -= siz;
        /* ignore MAXGAP when doing endgaps */
        siz = (-siz < MAXGAP || endgaps)? -siz : MAXGAP;
        i1++;
    }
    else if (siz > 0) { /* gap in first seq */
        pp[0].n[i0] = siz;
        pp[0].x[i0] = xx;
        gapx++;
        ngapx += siz;
        /* ignore MAXGAP when doing endgaps */
        siz = (siz < MAXGAP || endgaps)? siz : MAXGAP;
        i0++;
    }
}
else
    break;
}

/* reverse the order of jumps
*/
for (j = 0, i0--; j < i0; j++, i0--) {
    i = pp[0].n[j]; pp[0].n[j] = pp[0].n[i0]; pp[0].n[i0] = i;
    i = pp[0].x[j]; pp[0].x[j] = pp[0].x[i0]; pp[0].x[i0] = i;
}
for (j = 0, i1--; j < i1; j++, i1--) {
    i = pp[1].n[j]; pp[1].n[j] = pp[1].n[i1]; pp[1].n[i1] = i;
    i = pp[1].x[j]; pp[1].x[j] = pp[1].x[i1]; pp[1].x[i1] = i;
}
if (fd >= 0)
    (void) close(fd);
if (fj) {
    (void) unlink(jname);
    fj = 0;
    offset = 0;
}
}

```

FIGURE 248Q

```

/*
 * write a filled jmp struct offset of the prev one (if any): nw()
 */
writejumps(ix)
{
    int ix;
    char *mktemp();

    if (!fj) {
        if (mktemp(jname) < 0) {
            fprintf(stderr, "%s: can't mktemp() %s\n", prog, jname);
            cleanup(1);
        }
        if ((fj = fopen(jname, "w")) == 0) {
            fprintf(stderr, "%s: can't write %s\n", prog, jname);
            exit(1);
        }
    }
    (void) fwrite((char *)&dx[ix].jp, sizeof(struct jmp), 1, fj);
    (void) fwrite((char *)&dx[ix].offset, sizeof(dx[ix].offset), 1, fj);
}

```

writejumps

(30) 60/099,642	9 Sep/sep 1998 (09.09.1998)	US	(30) 60/101,472	23 Sep/sep 1998 (23.09.1998)	US	(30) 60/103,396	7 Oct/oct 1998 (07.10.1998)	US
(30) 60/099,741	10 Sep/sep 1998 (10.09.1998)	US	(30) 60/101,474	23 Sep/sep 1998 (23.09.1998)	US	(30) 60/103,401	7 Oct/oct 1998 (07.10.1998)	US
(30) 60/099,754	10 Sep/sep 1998 (10.09.1998)	US	(30) 60/101,475	23 Sep/sep 1998 (23.09.1998)	US	(30) 60/103,633	8 Oct/oct 1998 (08.10.1998)	US
(30) 60/099,763	10 Sep/sep 1998 (10.09.1998)	US	(30) 60/101,476	23 Sep/sep 1998 (23.09.1998)	US	(30) 60/103,678	8 Oct/oct 1998 (08.10.1998)	US
(30) 60/099,792	10 Sep/sep 1998 (10.09.1998)	US	(30) 60/101,477	23 Sep/sep 1998 (23.09.1998)	US	(30) 60/103,679	8 Oct/oct 1998 (08.10.1998)	US
(30) 60/099,808	10 Sep/sep 1998 (10.09.1998)	US	(30) 60/101,479	23 Sep/sep 1998 (23.09.1998)	US	(30) 60/103,711	8 Oct/oct 1998 (08.10.1998)	US
(30) 60/099,812	10 Sep/sep 1998 (10.09.1998)	US	(30) 60/101,738	24 Sep/sep 1998 (24.09.1998)	US	(30) 60/104,257	14 Oct/oct 1998 (14.10.1998)	US
(30) 60/099,815	10 Sep/sep 1998 (10.09.1998)	US	(30) 60/101,741	24 Sep/sep 1998 (24.09.1998)	US	(30) 60/104,987	20 Oct/oct 1998 (20.10.1998)	US
(30) 60/099,816	10 Sep/sep 1998 (10.09.1998)	US	(30) 60/101,743	24 Sep/sep 1998 (24.09.1998)	US	(30) 60/105,000	20 Oct/oct 1998 (20.10.1998)	US
(30) 60/100,385	15 Sep/sep 1998 (15.09.1998)	US	(30) 60/101,915	24 Sep/sep 1998 (24.09.1998)	US	(30) 60/105,002	20 Oct/oct 1998 (20.10.1998)	US
(30) 60/100,388	15 Sep/sep 1998 (15.09.1998)	US	(30) 60/101,916	24 Sep/sep 1998 (24.09.1998)	US	(30) 60/105,104	21 Oct/oct 1998 (21.10.1998)	US
(30) 60/100,390	15 Sep/sep 1998 (15.09.1998)	US	(30) 60/102,207	29 Sep/sep 1998 (29.09.1998)	US	(30) 60/105,169	22 Oct/oct 1998 (22.10.1998)	US
(30) 60/100,584	16 Sep/sep 1998 (16.09.1998)	US	(30) 60/102,240	29 Sep/sep 1998 (29.09.1998)	US	(30) 60/105,266	22 Oct/oct 1998 (22.10.1998)	US
(30) 60/100,627	16 Sep/sep 1998 (16.09.1998)	US	(30) 60/102,307	29 Sep/sep 1998 (29.09.1998)	US	(30) 60/105,693	26 Oct/oct 1998 (26.10.1998)	US
(30) 60/100,661	16 Sep/sep 1998 (16.09.1998)	US	(30) 60/102,330	29 Sep/sep 1998 (29.09.1998)	US	(30) 60/105,694	26 Oct/oct 1998 (26.10.1998)	US
(30) 60/100,662	16 Sep/sep 1998 (16.09.1998)	US	(30) 60/102,331	29 Sep/sep 1998 (29.09.1998)	US	(30) 60/105,807	27 Oct/oct 1998 (27.10.1998)	US
(30) 60/100,664	16 Sep/sep 1998 (16.09.1998)	US	(30) 60/102,484	30 Sep/sep 1998 (30.09.1998)	US	(30) 60/105,881	27 Oct/oct 1998 (27.10.1998)	US
(30) 60/100,683	17 Sep/sep 1998 (17.09.1998)	US	(30) 60/102,487	30 Sep/sep 1998 (30.09.1998)	US	(30) 60/105,882	27 Oct/oct 1998 (27.10.1998)	US
(30) 60/100,684	17 Sep/sep 1998 (17.09.1998)	US	(30) 60/102,570	30 Sep/sep 1998 (30.09.1998)	US	(30) 60/106,062	27 Oct/oct 1998 (27.10.1998)	US
(30) 60/100,710	17 Sep/sep 1998 (17.09.1998)	US	(30) 60/102,571	30 Sep/sep 1998 (30.09.1998)	US	(30) 60/106,023	28 Oct/oct 1998 (28.10.1998)	US
(30) 60/100,711	17 Sep/sep 1998 (17.09.1998)	US	(30) 60/102,684	1 Oct/oct 1998 (01.10.1998)	US	(30) 60/106,029	28 Oct/oct 1998 (28.10.1998)	US
(30) 60/100,919	17 Sep/sep 1998 (17.09.1998)	US	(30) 60/102,687	1 Oct/oct 1998 (01.10.1998)	US	(30) 60/106,030	28 Oct/oct 1998 (28.10.1998)	US
(30) 60/100,930	17 Sep/sep 1998 (17.09.1998)	US	(30) 60/102,965	2 Oct/oct 1998 (02.10.1998)	US	(30) 60/106,032	28 Oct/oct 1998 (28.10.1998)	US
(30) 60/100,848	18 Sep/sep 1998 (18.09.1998)	US	(30) 60/103,258	6 Oct/oct 1998 (06.10.1998)	US	(30) 60/106,033	28 Oct/oct 1998 (28.10.1998)	US
(30) 60/100,849	18 Sep/sep 1998 (18.09.1998)	US	(30) 60/103,449	6 Oct/oct 1998 (06.10.1998)	US	(30) 60/106,178	28 Oct/oct 1998 (28.10.1998)	US
(30) 60/101,014	18 Sep/sep 1998 (18.09.1998)	US	(30) 60/103,314	7 Oct/oct 1998 (07.10.1998)	US	(30) 60/106,248	29 Oct/oct 1998 (29.10.1998)	US
(30) 60/101,068	18 Sep/sep 1998 (18.09.1998)	US	(30) 60/103,315	7 Oct/oct 1998 (07.10.1998)	US	(30) 60/106,384	29 Oct/oct 1998 (29.10.1998)	US
(30) 60/101,071	18 Sep/sep 1998 (18.09.1998)	US	(30) 60/103,328	7 Oct/oct 1998 (07.10.1998)	US	(30) 60/108,500	29 Oct/oct 1998 (29.10.1998)	US
(30) 60/101,279	22 Sep/sep 1998 (22.09.1998)	US	(30) 60/103,395	7 Oct/oct 1998 (07.10.1998)	US	(30) 60/106,464	30 Oct/oct 1998 (30.10.1998)	US
(30) 60/101,471	23 Sep/sep 1998 (23.09.1998)	US				(30) 60/106,856	3 Nov/nov 1998 (03.11.1998)	US

(30) 60/106,902	3 Nov/nov 1998 (03.11.1998)	US	(30) 60/108,806	17 Nov/nov 1998 (17.11.1998)	US
(30) 60/106,905	3 Nov/nov 1998 (03.11.1998)	US	(30) 60/108,807	17 Nov/nov 1998 (17.11.1998)	US
(30) 60/106,919	3 Nov/nov 1998 (03.11.1998)	US	(30) 60/108,867	17 Nov/nov 1998 (17.11.1998)	US
(30) 60/106,932	3 Nov/nov 1998 (03.11.1998)	US	(30) 60/108,925	17 Nov/nov 1998 (17.11.1998)	US
(30) 60/106,934	3 Nov/nov 1998 (03.11.1998)	US	(30) 60/108,848	18 Nov/nov 1998 (18.11.1998)	US
(30) 60/107,783	10 Nov/nov 1998 (10.11.1998)	US	(30) 60/108,849	18 Nov/nov 1998 (18.11.1998)	US
(30) 60/108,775	17 Nov/nov 1998 (17.11.1998)	US	(30) 60/108,850	18 Nov/nov 1998 (18.11.1998)	US
(30) 60/108,779	17 Nov/nov 1998 (17.11.1998)	US	(30) 60/108,851	18 Nov/nov 1998 (18.11.1998)	US
(30) 60/108,787	17 Nov/nov 1998 (17.11.1998)	US	(30) 60/108,852	18 Nov/nov 1998 (18.11.1998)	US
(30) 60/108,788	17 Nov/nov 1998 (17.11.1998)	US	(30) 60/108,858	18 Nov/nov 1998 (18.11.1998)	US
(30) 60/108,801	17 Nov/nov 1998 (17.11.1998)	US	(30) 60/108,904	18 Nov/nov 1998 (18.11.1998)	US
(30) 60/108,802	17 Nov/nov 1998 (17.11.1998)	US			

